

**UTILITY
PATENT APPLICATION**

on

**METHODS TO CONSTRUCT MULTIMERIC DNA AND POLYMERIC
PROTEIN SEQUENCES AS DIRECT FUSIONS OR WITH LINKERS**

by

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METHODS TO CONSTRUCT MULTIMERIC DNA AND POLYMERIC PROTEIN SEQUENCES AS DIRECT FUSIONS OR WITH LINKERS

CROSS REFERENCE TO RELATED APPLICATIONS

5 This application claims priority to U.S. provisional application number US
60/396,466, filed July 16, 2002, naming Stuart Bussell as inventor.

SEQUENCE LISTING

10 A sequence listing is provided in electronic and printed form and as an appendix
to this application.

BACKGROUND

15 The present invention relates generally to recombinant DNA technology and
recombinant protein expression, and more specifically, to constructs comprising repeat
DNA sequences and to methods of making constructs comprising repeat DNA sequences,
including constructs that encode polymer peptides and proteins, in which monomers are
either fused directly or with linkers.

20 Recombinant proteins have become an important class of therapeutics and
diagnostics since their introduction in the 1980s. The first recombinant protein
therapeutics replaced products isolated from either animal or human tissue. For example,
recombinant human growth hormone (recombinant human GH or rhGH) replaced
material isolated from the pituitaries of human cadavers (Jorgenson, *Endocrine reviews*
12:189, 1991). The need arose because of the transmission of a rare fatal disease, called
Creutzfeldt-Jakob disease (CJD), that is transmitted from impurities in pituitary derived
hGH. The level of control possible with the recombinant version enabled production of
25 drug certifiably free of known communicable agents.

30 Another example of an early recombinant protein is recombinant human insulin
(rhI) (Chien, *Drug Development and Industrial Pharmacy* 22:753, 1996). In this case,
the recombinant product replaced, or supplemented, insulin isolated from the pancreases
from swine and cattle. The recombinant protein exactly matches the one found naturally
in humans, in contrast with the animal versions that differ by one to three amino acids.

More recombinant protein therapeutics followed including interferons, interleukins, hematopoietic factors, monoclonal antibodies, and others.

In the diagnostic field, antibodies, both natural and engineered, are used to recognize and signal the presence of clinical markers. An advantage of engineered antibody fragments over full-length antibodies is that they are amenable to production in facile expression systems such as *E. coli* or *P. pastoris* (Pennell et al., *Res Immunol* 149:599, 1998).

Some of the *in vivo* characteristics of recombinant drugs are described by their pharmacokinetic parameters. The field of pharmacokinetics concerns itself with the absorption, distribution, metabolism, and excretion (ADME) of compounds delivered *in vivo*. Basically, pharmacokinetic parameters describe the concentration of a drug distributed throughout the body over time.

Generally, absorption of protein drugs requires delivery by injection. A body's natural barriers tend to prevent the absorption of intact proteins if any other routes of delivery are used. The digestion system breaks down proteins administered orally, while the body's various epidermal surfaces prevent absorption throughout the body.

Once injected, proteins tend to distribute throughout the circulatory system where they can react (part of metabolism) with other molecules or undergo excretion. Mathematical models, of varying complexity, are available to explain experimental measurements of drug concentrations as a function of time. One of the basic pharmacokinetic parameters is a drug's half-life, $t_{1/2}$, which is characteristic of the drug's duration in the bloodstream.

A key determinant to a protein's half-life in the blood is its size, and this is a result of elimination of proteins from the blood by glomerular filtration in the kidneys (Venkatachalam et al., *Circulation Research* 43:337, 1978). Basically, the filtration allows proteins smaller than 60 kilodaltons (kD), and other similarly sized molecules, to pass out of the blood, resulting in urinary excretion, while retaining larger ones. This has a major impact on the dosing regimen for a given protein. Proteins smaller than 60 kD tend to need daily, or more frequent, injections.

One strategy to minimize the discomfort and inconvenience of daily injections is to prolong the action of proteins once introduced *in vivo*. Two basic strategies are used.

One involves the formulation of the protein into a slow release formulation (Putney et al., *Nature Biotechnology* 16:153, 1998). An example of this technique involves formulating proteins into a biocompatible polymer, poly lactic co-glycolytic acid (PLGA), that dissolves slowly over time, releasing protein during the dissolution process.

- 5 Recombinant hGH is one protein successfully formulated this way (Johnson et al., *Nature Medicine* 2:795, 1996). A disadvantage of this technique that complicates its widespread application is the challenge of formulating and manufacturing each protein so that it is stable during processing and use. Furthermore, injections of PLGA formulated proteins can be uncomfortable.

- 10 The other strategy to prolong a protein's *in vivo* action involves modifying the protein so that it acts like a larger particle and is excreted more slowly through the kidneys. While prolonging the proteins *in vivo* residence, the modification must avoid adverse consequences such as immunogenicity, toxicity, unwanted changes to the molecules distribution, and unwanted changes to its activity.

- 15 A common technique in protein modification involves conjugating a native protein to polyethylene glycol (PEG) or another protein (Roberts et al., *Adv Drug Deliv Rev* 54:459, 2002). PEG molecules are manufactured at all ranges of molecular weights. They can be attached to reactive chemical groups compatible with chemical conjugation to proteins, and they are safe *in vivo*. Pegylated proteins have been approved for human
20 use. Pegylated interferon is an example (Sharieff et al., *Cleve Clin J Med* 69:155, 2002). Pegylation effectively enhances the size of the resulting conjugate while avoiding immunogenicity or activity alterations. However, PEG has its own chemical and physical characteristics, and this can alter a conjugates ADME. For example, PEG alters the distribution of IL2 in such a way as to unacceptably increase its toxicity (Chen et al., *The*
25 *Journal of Pharmacology and Experimental Therapeutics* 293:248, 2000). Also, the chemical conjugation is difficult to completely control, and any resulting conjugate is likely to be a mix of chemical species.

- Another promising technique involves conjugating or fusing proteins to a carrier protein. There are many examples of chimeric molecules formed either through chemical
30 reaction between the parent proteins or through the fusion of their gene sequences. In the case of fusion proteins, experience shows that the separate polypeptides constituting a

fusion protein generally fold into their three dimensional conformation independently. In fact, often a recombinant protein that misfolds during expression in *E. coli* by itself will fold properly when fused to a protein that regularly folds correctly. Examples include fusions to commercially available proteins such as GST and NusA (see for example

5 Novagen, Madison, WI).

One technique to make therapeutic fusion proteins is to fuse native therapeutics to human serum albumin (HSA) (U.S. Pat. No. 5,876,969). HSA is a 66 kD protein that is abundant in the human bloodstream. It is non-immunogenic and readily available.

Potential problems include changed distribution of any resulting conjugate and the effect
10 of HSA as it is shuttled into cells that normally do not contain it intracellularly.

Another technique is to make therapeutic homomultimer fusion proteins. In this case, the coding DNA sequence for a functional protein is connected to copies of itself. A dimer of superoxide dismutase ("SOD") is disclosed in U.S. Pat. No. 5,084,390, whereby the hinge region of an immunoglobulin joins two copies of the SOD monomer.

15 The resulting dimer has an extended *in vivo* half-life. In another example, a dimer of erythropoietin is disclosed in U.S. Pat. No. 6,242,570.

Methods to manufacture highly polymerized sequences, for example polymers having greater than two units, have been developed in the field of artificial protein polymers. Lewis et al (*Protein Expression and Purification* 7:400, 1996) reveal a method
20 utilizing compatible, but nonregenerable, overhang restriction sites that are engineered to allow the polymerization of a monomeric spider silk repeating sequence in a geometric fashion. In similar manner, Elmorani, et al. (*Biochemical and Biophysical Research Communication* 239:240, 1997) use compatible, but nonregenerable, blunt end restriction sites to produce a polymeric form of wheat gliadin.

25 The techniques disclosed in both cases are predicated on the presence of a pair of compatible, nonregenerable, restriction sites at the end of the polymerizing protein sequence. This requirement severely limits the number of sequences that are amenable to polymerization. Another disadvantage of currently available methods is that once a final polymeric sequence is generated, the researchers must employ additional steps to
30 engineer it with the appropriate 5' and 3' sequences for expression.

SUMMARY OF THE INVENTION

The present invention provides methods to easily and quickly generate multimers, such as dimers and higher order multimers, of DNA sequences and their open reading
5 frame protein translations, resulting in constructs for the expression of proteins of greater molecular weight and valency. Methods are described whereby a sequence is attached to one or more versions of itself, either via a direct fusion or with a linker, where each version shares strong homology and is generally considered the same via its sequence and mode of action. In addition, the multimer is attached to terminal functional elements.

10 The monomer can theoretically have any sequence and can consist of elements from one or more genes or synthetic DNA fragments. Thus, although the polymerization employs homomultimers, the fundamental monomers themselves can be generated from heterogeneous sequences. Furthermore, heteromultimers can be produced from monomers previously manipulated with the methods of this invention if the constitutive
15 monomers have compatible ends.

In one aspect, the present invention comprises multimer assemblies of cassettes that comprise nucleic acid sequences having restriction sites that can be ligated together to form constructs (multimer cassettes) having multiple copies of a sequence of interest (the monomer sequence), such as a sequence that encodes a peptide or protein.

20 Restriction sites used to ligate cassettes of a multimer assembly together to make a multimer cassette comprise restriction pair members that when ligated together, do not regenerate a restriction site. In one embodiment of the present invention, multimer assemblies are used that comprise 1) at least one amplification cassette comprising at least a monomer sequence and 2) at least one 3'-terminal cassette comprising at least one
25 3' specific sequence or at least one 5'-terminal cassette comprising at least one 5' specific sequence. Preferably, the 5'-terminal and/or 3'-terminal cassettes additionally comprise at least a portion of the monomer sequence.

In some preferred embodiments of this aspect of the invention, component cassettes (such as amplification cassettes, 5'-terminal and/or 3'-terminal cassettes) of a
30 multimer assembly can comprise one or more flanking restriction sites that can facilitate cloning of multimer cassettes.

In some preferred embodiments, component cassettes (such as amplification cassettes, 5'-terminal and/or 3'-terminal cassettes) can comprise one or more linker sequences, such as linker sequences that encode amino acids or peptides that can be used to link monomers. Such linker sequence can also comprise restriction sites, such as
5 restriction pair members that can be used in making multimer cassettes.

In another aspect, the present invention provides methods of making multimer cassettes. Such methods include ligation of 3' and 5' restriction pair members of component cassettes. In some preferred embodiments, the synthesis of multimer cassettes can optionally make use of flanking restriction sites that can be provided in the
10 component cassettes. In some preferred embodiments, the synthesis of multimer cassettes can optionally make use of restriction sites that can be provided in linker sequences included in one or more component cassettes.

The protein polymers encoded by DNA multimers of a multimer cassette can be expressed in any suitable gene/protein expression system. For example, prokaryotic or
15 eukaryotic systems are suitable, as are *in vitro* translation systems. The multimer assembly system described here facilitates the multimerization process and enables the production of multimers of any size and with a variety of N-terminal, linker, and C-terminal elements from a limited number of starting DNA sequences. For example, a gene can be designed for intracellular expression with an N-terminal methionine and for
20 extracellular expression by including a secretory signal sequence after the N-terminal methionine.

The invention can be used to produce constructs having multimeric or polymeric sequences of increased size and multiplicity.

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BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a diagram showing an example of a multimer assembly and its cassettes for monomers having a terminal restriction pair. **(A)** shows a 5'-terminal cassette with sequence elements coding for protein N-terminal elements. The crosshatched elements are restriction sites, the rectangular segments are portions of the monomer sequence, the looping arrows indicate continuation as a plasmid, straight arrows indicate linker sequences, and ~ refers to arbitrary DNA sequences. The circle is a start codon, and the square is a 5' specific sequence. Restriction site 1 can include the start codon and/or can be a flanking restriction site for cloning flexibility. Restriction site 3 is the 3' restriction pair member, and 2 and 4 are flanking restriction sites for cloning flexibility. **(B)** shows an amplification cassette with sequence elements coding for a polymerizing sequence. Restriction site 5 is the 5' restriction pair member. **(C)** shows a 3'-terminal cassette with sequence elements coding for C-terminal elements. The pentagon represents 3' specific sequence and the hexagon a stop codon. The restriction site arrangement is preferred, but not the only arrangement for construction of an insert cassette. **(D)** shows one example of a Linker sequence. As shown here, it can contain elements 5' and 3' of the restriction pair formed by ligating restriction sites 5 and 3 together. The left and right arrows represent linker 5' and 3' elements, respectively.

Fig. 2 is a diagram showing one example of a multimer assembly and its cassettes for a monomer with an internal restriction pair. The crosshatched elements are restriction sites, the rectangular segments are portions of the monomer sequence, the looping arrows indicate continuation as a plasmid, straight arrows indicate linker sequences, and ~ refers to arbitrary DNA sequences. The circle is a start codon, and the square is a 5' specific sequence. The pentagon represents 3' specific sequence and the hexagon a stop codon. **(A)** shows a 5'-terminal cassette with sequence elements coding for N-terminal elements. **(B)** shows an amplification cassette with sequence elements coding for the polymerizing sequence. The double arrow represents a linker (optional). **(C)** shows a 3'-terminal cassette with sequence elements coding for C-terminal elements. **(D)** shows an

alternative 3'-terminal cassette that requires use of sequential ligation to form a multimer expression cassette.

Fig. 3 is a diagram showing two examples of pathways that can be used in the

- 5 polymerization of amplification cassettes. Both procedures depicted involve two generalized cassettes, one with insert sequence b1 and the other with insert sequence b2. For pathway A, the b2 containing cassette is opened by digesting with enzymes 1 and 5. The b1 insert sequence is isolated after digesting the b1 containing cassette with enzymes 1 and 3. For pathway B, the b1 containing cassette is opened by digesting with enzymes 10 2 and 3. The b2 insert sequence is isolated after digesting the b2 containing cassette with enzymes 2 and 5. The final ligations to generate multimer assemblies are similar for both cases. The crosshatched elements are restriction sites, the rectangular segments are insert sequences, the looping arrows indicate continuation as a plasmid, and ~ refers to arbitrary DNA sequences.

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Fig. 4 is a diagram showing examples of sequential ligation of cassettes to create a functional multimer cassette of a desired size. The schematic is a generalization of the sequential ligation procedure necessary for use with a 3'-terminal cassette given in Figure 2D. Pathway A depicts the insertion of an 'S' plasmid fragment into a 'T' containing 20 plasmid, while Pathway B depicts the insertion of a 'T' plasmid fragment into a 'S' containing plasmid. In the figure, $S + T = 5I + AI$, $AI + 3I$, $5IAI + 3I$, or $5I + AI3I$, where $5I \equiv$ the insert from a 5'-terminal cassette, $AI \equiv$ the insert from an amplification cassette, $3I \equiv$ the insert from a 3'-terminal cassette, $5IAI \equiv$ the insert resulting from the ligation of $5I$ and AI , $AI3I \equiv$ the insert resulting from the ligation of AI with $3I$, and $5IAI3I \equiv$ the 25 insert resulting from the ligation of $5I$ with $AI3I$ or $5IAI$ with $3I$. Formation of $5IAI3I$ requires two sequential ligations and generation of intermediate $5IAI$ or $AI3I$ cassettes for each polymer size made. The crosshatched elements are restriction sites, the rectangular segments are insert sequences, the looping arrows indicate continuation as a plasmid, and ~ refers to arbitrary DNA sequences.

30

Fig. 5 is a diagram showing possible methods for generation of an insertion cassette.

Pathways A and B are alternative pathways for insertion cassette generation based on different arrangements of flanking restriction sites. Pathway A involves opening the 5'-terminal cassette and inserting a fragment from the 3'-terminal cassette, while Pathway B involves opening the 3'-terminal cassette and inserting a fragment from the 5'-terminal cassette. The crosshatched elements are restriction sites, the rectangular segments are portions of the monomer sequence, the looping arrows indicate continuation as a plasmid, straight arrows indicate linker sequences, and ~ refers to arbitrary DNA sequences. The circle is a start codon, and the square is a 5' specific sequence. The pentagon represents 3' specific sequence and the hexagon a stop codon.

Fig. 6 is a diagram showing one possible method of generating a functional multimer cassette of a desired size from an insertion cassette and an amplification cassette. The insertion cassette is opened at both sites of the restriction pair with subsequent ligation of the insert from an amplification cassette, but the insert can ligate in the wrong orientation. Correct inserts must be identified by subsequent analysis. The crosshatched elements are restriction sites, the rectangular segments are portions of the monomer sequence, the looping arrows indicate continuation as a plasmid, straight arrows indicate linker sequences, and ~ refers to arbitrary DNA sequences. The circle is a start codon, and the square is a 5' specific sequence. The pentagon represents 3' specific sequence and the hexagon a stop codon.

Fig. 7 is a diagram showing another possible method of generating a functional multimer cassette of a desired size from an insertion cassette and an amplification cassette. The insertion cassette is opened with enzymes 3 and 2 to create an oriented ligation, but an additional step is required. In this case, the amplification cassette has flanking restriction site 2 on the 3' side of restriction site 3. The crosshatched elements are restriction sites, the rectangular segments are portions of the monomer sequence, the looping arrows indicate continuation as a plasmid, straight arrows indicate linker sequences, and ~ refers to arbitrary DNA sequences. The circle is a start codon, and the square is a 5' specific sequence. The pentagon represents 3' specific sequence and the hexagon a stop codon.

Fig. 8 is a diagram showing another possible scheme for generating a functional multimer cassette of a desired size from an insertion cassette and an amplification cassette in similar fashion to **Figure 7**, but the amplification cassette has flanking restriction site 2 on the 5' side of restriction site 5.

Fig. 9 is a diagram showing the PCR amplification of the hGH gene, its subsequent ligation to generate p0A0, and the ligation of the OmpA leader sequence to generate p0C0A2.

Fig. 10 is a diagram showing the PCR mutagenesis of the hGH gene to generate p0A01. The diagram also shows the ligation of the OmpA sequence into p0A01 to generate p0A11A2 and the ligation of the PstI/BamHI fragment from p0A01 into P0A03 to generate p0A11A1.

Fig. 11 is a diagram showing the PCR mutagenesis of the hGH gene to generate p0A11B.

Fig. 12 is a diagram showing the ligation of synthetic sequences to generate p0A11C1 and p0A11C2.

Fig. 13 is diagram showing the polymerization of a GH direct fusion amplification cassette.

Fig. 14 is diagram showing the generation of the GH direct fusion insertion cassette, p0A11D, and subsequent ligation of an amplification cassette to generate a multimer expression cassette.

Fig. 15 is a diagram showing the PCR mutagenesis of the hGH gene to generate p0A21B, the base amplification cassette for the GH glycine linker assembly.

Fig. 16 is a diagram showing the PCR mutagenesis of the hGH gene to generate the base cassettes, p0A31A, p0A31B, and p0A31C, for the GH SWG₄S assembly.

Fig. 17 is a diagram showing the sequential ligation of the GH SWG₄S assembly
5 cassettes to generate the multimer expression cassette, p0A31E3.

Fig. 18 is a picture of an SDS-PAGE gel showing the separation of proteins by molecular weight from separate lysates from cells expressing different polymers of rhGH. Lane 1 contains molecular weight standards, lane 2 the rhGH monomer, lane 3 the rhGH dimer,
10 lane 4 the rhGH trimer, lane 5 the rhGH pentamer, and lane 6 the rhGH nanamer.

Fig. 19 is a diagram showing insertion of synthetic sequences to generate the G₄S assembly 5'-terminal and amplification cassettes.

15 **Fig. 20** is a diagram showing PCR mutagenesis of the hGH gene to generate p0A04 and p0A41C.

Fig. 21 is a diagram showing ligation of the insert from p0D13A with p0A04 to generate p0A43B and ligation of the PstI/EcoRI fragment from p0A11A1 to generate p0A43A.

20 **Fig. 22** is a diagram showing ligations to generate the base cassettes; p0A51A, p0A51B, and p0A51C, for the GH direct fusion assembly utilizing blunt ended HindIII and NcoI sites for the restriction pair.

25 **Fig. 23** is a diagram showing the polymerization of the p0A51B insert to generate p0A51B2.

DETAILED DESCRIPTION OF THE INVENTION

Introduction

The current invention discloses methods that extend the polymerization techniques in three important ways. First, it introduces new methods to generate highly polymerized sequences from monomers that are incompatible with previous protein polymerization techniques. Second, it introduces additional linker sequences that, when paired with the monomer sequences, facilitate their use. Third, it introduces methods that facilitate the construction and expression of functional multimers and polymers. Taken together, the new methods enable the generation of large numbers of polymer variants that can differ in sequence and degree of polymerization. These variants can then be tested for desirable traits.

The disclosed techniques are applicable to any polypeptide sequence and can prove useful for proteins for which increased total molecular weight is deemed advantageous. The disclosed techniques are also useful for proteins for which increased valency is deemed advantageous. For example, expression of single chain antibody fragments fused together as larger multimers have the advantage of high valency and a stable linkage. Furthermore, if cassettes for two different sequences share compatible restriction pair members, they can be co-polymerized to produce heteromultimers.

20 Definitions

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Conventional methods are used for these procedures, such as those provided in the art and various general references. Where a term is provided in the singular, the inventors also contemplate the plural of that term. The nomenclature used herein and the laboratory procedures described below are those well known and commonly employed in the art. Where there are discrepancies in terms and definitions used in references that are incorporated by reference, the terms used in this invention shall have the definitions given herein. As employed throughout the disclosure, the following terms, unless otherwise indicated, shall be understood to have the following meanings:

Monomer. A DNA or amino acid sequence whose polymerization is desirable. A monomer can be a portion of a naturally occurring sequence (for example, a binding domain of an antibody). The sequence can be derived from one or more naturally occurring ones, or can be a synthetic sequence, or can be any combination of sequences of synthetic and natural origins. Monomers of the present invention can comprise linkers. As used herein monomer sequence means a nucleic acid sequence.

Multimer. A nucleic acid sequence encoding two or more monomers.

10 Polymer or Multimeric protein. A functional polypeptide that can be synthesized from a multimer assembly of the present invention. A polymer comprises at least two monomers (where each monomer can optionally comprise one or more linkers), can comprise one or more 5' translated regions (for example, signal peptides, N-terminal regions, "pro" or "pre" protein sequences, tag sequences, etc.), and can comprise one or more 3' translated regions (for example, C-terminal regions, tag sequences, etc.)

20 Linker. A linker is a DNA or amino acid sequence that connects one DNA sequence with another through covalent bonds or an amino acid or peptide that connects one peptide or protein unit with another peptide or protein unit through peptide bonds. An amino acid or peptide linker can be a single amino acid (for example, glycine) or can be more than one amino acid.

25 Restriction Pair. Two restriction sites that have different recognition sequences that are ligation compatible, but when ligated together do not regenerate either of the two original restriction sites. A restriction pair can include two restriction sites that have overhangs, such as BglII and BamHI, or can include any two blunt end restriction sites that do not have the same recognition sequence, such as StuI and NaeI. In a broader application, a restriction pair can also include restriction sites that are initially ligation incompatible but are blunt ended to make them ligation compatible. An example includes blunt ending

30 HindIII and NcoI to make them ligation compatible.

Restriction pair member or restriction member. A restriction site that is part of a restriction pair. The 5' and 3' restriction pair members together make up a restriction pair, and each is the other's partner.

5 5' restriction pair member or 5' restriction member or 5' member. A restriction pair member that is located at the 5' terminus of a DNA sequence, such as a DNA sequence that, at least in part, encodes a monomer whose multimerization is desired or multimer of the present invention, or is located at the 5' terminus of a DNA sequence of interest whose ligation to a multimer is desired. The term "5' restriction pair member" or "5'
10 member" can be used to refer to an unaltered restriction site (for example, a Bam HI site) or to a restriction site that has been altered, such as, for example, a filled-in 5' restriction pair member (such as blunt ended Bam HI site), or a fused 5' restriction pair member (for example, a ligated BamHI/BglII site).

15 3' restriction pair member or 3' restriction member or 3' member. A restriction pair member that is located at the 3' terminus of a DNA sequence, such as a DNA sequence that, at least in part, encodes a monomer whose multimerization is desired or multimer of the present invention, or is located at the 3' terminus of a DNA sequence of interest whose ligation to a multimer is desired. The term "3' restriction pair member" or "3'
20 member" can be used to refer to an unaltered restriction site (for example, a BglII site) or to a restriction site that has been altered, such as, for example, a filled-in 3' restriction pair member (such as blunt ended BglII site), or a fused 3' restriction pair member (for example, a ligated BamHI/BglII site).

25 Flanking restriction site or flanking site. A restriction site that is not a member of a restriction pair used in the constructs and methods of the present invention. Its location outside of insert sequences and restriction pair members used in the cassettes and methods of the present invention can facilitate manipulation of the insert.

Insertion restriction site. A specific flanking restriction site that is 3' of the 3' restriction pair member of the 5'-terminal cassette and 5' of the 5' restriction pair member of the 3'-terminal cassette.

- 5 Amplification cassette. A DNA sequence that includes at least one monomer that is flanked by a restriction pair. An amplification cassette has a 5' restriction pair member at its 5' terminus and a 3' restriction pair member at its 3' terminus. The restriction pair enables the multimerization of the sequence or the ligation of it to other sequences with ligation compatible restriction sites. An amplification cassette can optionally comprise
10 other sequences as well, such as but not limited to sequences that code for amino acid or peptide linkers.

- 5'-terminal cassette. A DNA sequence that comprises a 3' restriction pair member, at least one 5'-specific sequence, where a 5'-specific sequence is a sequence that, when
15 positioned at the 5' end of a multimer sequence, can facilitate the use of DNA multimers or the expression, purification, or identification of at least one protein polymer of the present invention, and, preferably, at least a portion of a monomer sequence. The 3' restriction pair member is ligation compatible with the 5' terminus of at least one amplification cassette. The 5'-terminal cassette is useful for introducing 5'-terminal
20 DNA sequences that contribute to making a sequence functional. Examples of 5' specific sequences include, but are not limited to, the translation start codon, secretion sequences, tag sequences, linker sequences, or special restriction sites.

- 3'-terminal cassette. A DNA sequence that comprises a 5' restriction pair member, at
25 least one 3'-specific sequence, where a 3'-specific sequence is a sequence that, when positioned at the 3' end of a multimer sequence, can facilitate the use of DNA multimers or the expression, purification, or identification of at least one protein polymer of the present invention, and, preferably, at least a portion of a monomer sequence. The 5' restriction pair member is ligation compatible with the 3' terminus of at least one
30 amplification cassette. The 3'-terminal cassette is useful for introducing 3'-terminal DNA sequences that contribute to making a sequence functional. Examples of 3' specific

sequences include, but are not limited to, tag sequences, C-terminal sequences, polyadenylation sequences, stop codons, linker sequences, and the like.

Insert sequence. The functional sequence in a cassette. For the amplification cassette, the functional sequence includes both restriction pair members and all sequence in between, including the monomer sequence. For the 5'-terminal cassette, the functional sequence includes the 3' restriction pair member, all 5'-specific sequences, and its portion of a monomer sequence, if present. For the 3'-terminal cassette, the functional sequence includes the 5' restriction pair member, all 3'-specific sequences, and its portion of a monomer sequence, if present. For multimer cassettes, the functional sequence includes the functional sequences of the constitutive cassettes.

Multimer assembly. The collection of all cassettes that, in combination, after ligation, yields functional multimer DNA sequences or polymer protein sequences of a starting monomer. A multimer assembly comprises one or more 5'-terminal cassettes and one or more amplification cassettes; one or more amplification cassettes and one or more 3'-terminal cassettes; or one or more 5'-terminal cassettes, one or more amplification cassettes, and one or more 3'-terminal cassettes that can be fused using 3' and 5' restriction pair members.

Multimer cassette. A cassette resulting from the ligation of two or more cassettes from the same multimer assembly.

Insertion Cassette. A multimer cassette generated from the ligation of a 5'-terminal and 3'-terminal cassette of a multimer assembly that is ligation compatible with any of said assembly's amplification cassettes to generate a multimer cassette.

Multimer expression cassette. A multimer cassette that, when transcribed and translated in a suitable expression system, produces a polymer protein sequence of a starting monomer.

Segment of a monomer sequence. A segment of a monomer sequence is a portion of monomer sequence, that is, a nucleic acid sequence that encodes a portion of a monomer.

I. METHODS OF MAKING MULTIMER ASSEMBLIES

5

The present invention includes methods of fusing two or more nucleic acid sequences. The nucleic acid sequences can encode for peptide or protein sequences, such that when the nucleic acid sequences are expressed, a polymeric protein is produced. Preferably, in the methods of the present invention, the peptide or protein monomers
10 encoded by the nucleic acid sequences are identical peptide or protein monomers. However, this is not a requirement of the present invention. The nucleic acid sequence, whose polymerization is desired is called a monomer sequence.

Monomer sequences can encode proteins or peptides whose function is known or unknown. Preferably, however, the identity and function of the peptide or protein
15 encoded by a monomer sequence is known. Of particular interest are peptides and proteins that can have diagnostic or therapeutic value (for example, human growth hormone, hGH), although the invention is not limited to these protein sequences.

For example, monomer sequences can encode at least a portion of one or more receptors, receptor ligands, enzymes, inhibitors, transcription factors, translation factors,
20 DNA replication factors, activators, chaperonins, or antibodies. Monomer sequences can also encode at least a portion of one or more cytokines, growth factors, or hormones such as, but not limited to, Interferon-alpha, Interferon-beta, Interferon-gamma, Interleukin-1, Interleukin-2, Interleukin-3, Interleukin-4, Interleukin-5, Interleukin-6, Interleukin-7, Interleukin-8, Interleukin-9, Interleukin-10, Interleukin-11, Interleukin-12, Interleukin-
25 13, Interleukin-14, Interleukin-15, Interleukin-16, Erythropoietin, Colony-Stimulating Factor-1, Granulocyte Colony-stimulating Factor, Granulocyte-Macrophage Colony-Stimulating Factor, Leukemia Inhibitory Factor, Tumor Necrosis Factor, Lymphotoxin, Platelet-Derived Growth Factor, Fibroblast Growth Factors, Vascular Endothelial Cell Growth Factor, Epidermal Growth Factor, Transforming Growth Factor-beta,
30 Transforming Growth Factor-alpha, Thrombopoietin, Stem Cell Factor, Oncostatin M, Amphiregulin, Mullerian-Inhibiting Substance, B-Cell Growth Factor, Macrophage

Migration Inhibiting Factor, Endostatin, and Angiostatin. Descriptions of these proteins can be found in Human Cytokines: Handbook for Basic and Clinical Research, Aggarwal, B. B. and Gutterman, J. U. Eds., Blackwell Scientific Publications, Boston, Mass., (1992), which is herein incorporated by reference in its entirety.

5 The monomer encoding sequences are polymerized together by ligation of compatible, nonregenerable restriction sites, called restriction pair members. Unlike previous methodologies, the present invention employs cassettes with sequences other than those encoding the original monomer itself in the construction process. For example:

10 In the methods of the present invention, multimer assemblies are used that comprise at least one amplification cassette and at least one of the following: at least one 3'-terminal cassette or at least one 5'-terminal cassette. An amplification cassette comprises an insert sequence that includes a monomer sequence whose polymerization is desired, a 5' restriction pair member at its 5' terminus, and a 3' restriction pair member at
15 its 3' terminus. A 3'-terminal cassette comprises an insert sequence that includes at least one 3' specific sequence and a 5' restriction pair member site that can be fused to a 3' restriction pair member site of at least one of the one or more amplification cassettes. A 5'-terminal cassette, comprises an insert sequence that includes at least one 5' specific sequence and a 3' restriction pair member site that can be fused to a 5' restriction pair
20 member site of at least one of the one or more amplification cassettes. Preferably, the 5'-terminal and/or 3'-terminal cassettes additionally comprise at least a portion of the monomer sequence.

 5' specific sequences can be, but are not limited to, sequences that enhance transcription, translation, secretion, protein folding, protein solubility, or binding of the
25 protein to specific binding members such as antibodies. 3' specific sequences can be, but are not limited to, stop codons or sequences that enhance RNA stability, protein folding, protein solubility, or binding of the protein to specific binding members such as antibodies.

 In the multimer assemblies of the present invention, 5' and 3' restriction pair
30 members are used to fuse amplification cassettes, and preferably, where applicable, 3'-terminal cassettes to amplification cassettes and 5'-terminal cassettes to amplification

cassettes. 5' and 3' restriction pair members are preferably unique restriction sites that are ligation compatible, and said ligation destroys each member. In the alternative, 5' and 3' restriction pair members can be ligation incompatible sites that are made ligation compatible by blunt ending.

5 One aspect of the present invention is construction of cassettes comprising one or more flanking restriction sites that aid their use, but this is not a requirement of the present invention. Preferably, 3'-terminal cassettes and 5'-terminal cassettes, if present, comprise 3' and 5' flanking restriction sites. Flanking restriction sites can be any restriction site (except restriction pair member sites used in the same construct), and
10 preferably aid the use of cassettes by increasing the facility of making multimer cassettes. For example, the flanking sites facilitate the manipulation of the insert sequences, including their isolation and ligation. For example, some preferred methods employ an insertion restriction site, which is a specific flanking restriction site that is 3' of the 3' restriction pair member of the 5'-terminal cassette and 5' of the 5' restriction pair
15 member of the 3'-terminal cassette. Flanking restriction sites can also optionally be used to transfer constructs and assemblies to different expression vectors

 In some preferred methods of the invention, sequences encoding linkers are employed. Multimer assembly cassettes can comprise one or more linker sequences. Multimer assembly cassettes can have linker sequences 5' of one or more insert
20 sequences, 3' of one or more insert sequences, or both 5' and 3' of one or more insert sequences. Linker sequences can be part of amplification cassettes, 5'-terminal cassettes, 3'-terminal cassettes, or any combination thereof. In preferred aspects of the present invention, nucleic acid sequences that encode amino acid or peptide linkers that are used to link monomers can also comprise restriction sites, such as 3' or 5' restriction pair
25 member sites that can facilitate construction of multimer assemblies. This provides a convenient means for introducing restriction pair members for efficient polymerization of monomer sequences through amplification cassettes and optionally 5'-terminal cassette or 3'-terminal cassette ligations. Alternatively, or in addition, amino acid or peptide linkers can be used to provide optimal spacing or folding of translated monomers or a
30 polymer.

Where more than one linker sequence is used in a single multimer assembly cassette, they may or may not occur between each and every monomer sequence. Where more than one linker sequence is used in a single multimer assembly cassette, they can encode the same or different amino acid or peptide linkers.

5 Peptide linkers are well known in the art. Preferably linkers are between one and twenty amino acids in length, and more preferably between one and ten amino acids in length, although length is not a limitation in the linkers of the present invention. Preferably linkers comprise amino acid sequences that do not interfere with the conformation and activity of peptides or proteins encoded by monomers of the present
10 invention. Some preferred linkers of the present invention are those that include the amino acid glycine. Examples include those disclosed in **Table 1**.

 In an expressed protein polymer, such amino acid or peptide sequences join peptide or protein monomer sequences. If a linker is part of the insert sequence of the amplification cassette, it becomes part of the monomer that is to be multimerized. The
15 linker sequence can comprise at least one restriction pair member.

 The present invention also introduces several methods to expand the use of restriction pair member sites. For example:

 In some methods of the present invention, restriction pair members that are used to join monomer sequences are internal to a monomer sequence. In these embodiments, an
20 amplification cassette comprises a 5' segment of a monomer sequence and a 3' segment of a monomer sequence that together comprise the sequence of a complete monomer. The 5' segment is positioned 3' of the 3' segment, the 5' terminus of the 3' segment is a 5' restriction pair member, and the 3' terminus of the 5' segment is a 3' restriction pair member. In this case, in making a multimer cassette, ligation of the 3' restriction pair
25 member of the 5' segment of one amplification cassette with the 5' restriction pair member of the 3' segment of another amplification cassette can form a complete monomer sequence. In order to complete the polymer sequences, a multimer assembly preferably comprises a 5'-terminal cassette that comprises the 5' monomer segment and a 3'-terminal cassette that comprises the 3' monomer segment. In this way, monomer
30 sequences provided in the amplification cassettes can be provided in non-contiguous segments. In some preferred methods of the present invention, the amplification cassette

further comprises a linker that is positioned between the 5' segment and the 3' segment of the monomer sequence.

In some methods of the present invention, restriction pair members can be overhang restriction sites. In some methods of the present invention, restriction pair members can be blunt end restriction sites. In some other methods of the present invention, restriction pair members are incompatible "overhang" restriction sites that are converted to blunt end restriction sites through the use of polymerases or nucleases.

In some preferred methods of the present invention, restriction pair members are conveniently provided in one or more linker sequences. In these embodiments, linker sequences comprising a restriction pair member can be engineered onto the 3', 5', or both ends of an insert sequence.

In some preferred methods of the present invention, the 3'-restriction pair member codes for a stop codon that is destroyed upon ligation to the 5'-restriction pair member.

In one aspect of the present invention, the assembly methodology consists of the following four steps:

1. Generate or obtain the DNA for the monomer.

Techniques familiar to those skilled in the art include, but are not limited to:

- a. Amplification of a sequence from a DNA library, optionally including any additions or mutations to the sequence in PCR primers.
- b. Chemical synthesis of the sequence
- c. Splicing of sequences together from pre-existing DNA

2. Decide what linker sequence, if any, to use between monomers and construct a multimer assembly.

Options for the linker include none (direct fusion of monomers), a linker encompassing a restriction pair member within its sequence, a linker with restriction pair members at one or more termini, or a linker lacking a restriction pair member. Once a linker is added, it becomes part of the monomer sequence.

For each option, three basic cassettes can be generated: one or more 5'-terminal cassettes, at least one amplification cassette, and one or more 3'-terminal cassettes.

However, in some instances, all three cassettes are not required. A multimer assembly comprises at least one amplification cassette, and one or more 5'-terminal cassettes or one or more 3'-terminal cassettes, or can have at least one amplification cassette, one or more 5'-terminal cassettes, and one or more 3'-terminal cassettes. In some cases, multiple versions of each cassette may be desirable. Furthermore, the amplification cassette can be polymerized to produce new higher order (multimeric) amplification cassettes.

The ends of the monomers determine the characteristics of the cassettes. The current invention discloses the use of linkers to introduce ends containing a restriction pair as well the construction of 5'-terminal and/or 3'-terminal cassettes to facilitate their use.

As an alternative to engineering the ends of a monomer with a restriction pair, then the cassettes can be constructed with a restriction pair internal to the monomer sequence. The construction of the cassettes is modified to accommodate the presence of a noncontiguous monomer in each.

Finally, a method is disclosed in which the constructions for a restriction pair either at the ends or internal to the monomer is extended to use with a pair of incompatible restriction sites. This method is less preferred, as the method requires that blunt ends for ligation are created for each ligation step (by nuclease digestion or polymerase fill-in, or both), decreasing the efficiency of the procedure.

The following are the general steps for construction of the assemblies for each possible restriction pair case:

a. Using a monomer sequence with a terminal restriction pair.

The scheme shown in **Figure 1** is applicable for any monomer sequence that can be engineered with a terminal restriction pair. The steps to engineer the assembly can include the following:

(1) Engineer 5'-terminal cassettes containing one or more 5' specific DNA sequences (for example, start codon, secretion sequence, etc.), preferably the monomer sequence, linker sequence, if present, and the 3' member of the restriction pair.

(2) Engineer an amplification cassette containing a 5' restriction member, optionally a first linker sequence, at least one monomer sequence, optionally a second linker sequence, and a 3' restriction member.

(3) Engineer 3'-terminal cassettes containing a 5' restriction member, optionally a linker sequence, preferably the monomer sequence, and one or more 3'-terminal specific DNA sequences (specific recognition sequences, stop codon, etc.).

5 An alternative formulation involves 5'-terminal and/or 3'-terminal cassettes that do not include any monomer sequence. The utility of including the monomer sequence in both terminal cassettes lies in utilizing the restriction pair members to join each terminal cassette to an amplification cassette, however, this is not a requirement of the present invention.

10

b. Using a monomer sequence with an internal restriction pair.

The scheme shown in **Figure 2** is applicable for any monomer sequence that can be engineered with an internal restriction pair. The steps to engineer the assembly include the following:

15 (1) Engineer 5'-terminal cassettes containing one or more 5' specific DNA sequences (start codon, secretion sequence, etc.), the portion of a monomer sequence that occurs on the 5' side of the restriction pair (the 5' monomer segment), and finally the 3' restriction pair member.

(2) Engineer an amplification cassette containing a 5' restriction pair member, DNA
20 encoding the portion of a monomer sequence that occurs 3' of the restriction pair (the 3' monomer segment), optionally a linker sequence, DNA encoding the portion of a monomer that occurs 5' of the restriction pair (the 5' monomer segment), and a 3' restriction pair member.

(3) Engineer 3'-terminal cassettes containing the 5' restriction pair member, the portion
25 of a monomer sequence that occurs 3' of the restriction pair (the 3' monomer segment), and one or more 3'-terminal specific DNA sequences (specific recognition sequences, stop codon, etc.).

c. Using a monomer sequence with a pair of incompatible restriction sites made
30 compatible by blunt ending.

Either scheme shown in **Figure 1** or **Figure 2** are applicable, but in this case the restriction pair consists of restriction sites that are blunt ended to make them compatible.

Once constructed, the amplification cassette enables generation of a sequence containing any number of monomers fused together.

5

3. Polymerize the amplification cassette in an arithmetic, geometric, or mixed progression (see **Figure 3**).

10 A series of amplification cassettes are generated from the original amplification cassette. The technique involves digesting a first construct comprising an amplification cassette at two 5' or two 3' sites of an insert, one of which is a restriction pair member site and the other of which is an external flanking site (external to the restriction pair member site), to open up the construct. This is followed by digesting a second construct comprising an amplification cassette at the same flanking site, but with the opposite restriction pair member, to release the amplification sequence from the plasmid as a
15 fragment. This sequence is then ligated into the opened first plasmid construct from before. Both restriction sites used in the ligation are destroyed, but the resulting cassette has intact flanking restriction sites and an intact restriction pair on the ends that enable further polymerizations.

Mixing and matching the cassettes used to open a construct that comprises an
20 amplification cassette and to generate an insert from a construct that comprises an amplification cassette enables new cassettes of any size to be made in an arithmetic, geometric, or mixed progression. For example, if the monomer is used to both open the plasmid and create insert, a dimer cassette is made. If the resulting dimer is used for both, then a tetramer is made. If this tetramer is used for both, then an octamer is made,
25 and continuation leads to a binomial geometric progression. On the other hand, if the monomer is always used as the insert and the newest cassette is used to receive the insert, an arithmetic progression of one is produced. For instance, when a dimer construct is opened and a monomer fragment inserted, then a trimer is produced. When a trimer construct is opened and a monomer fragment is inserted, then a tetramer is produced. In
30 general, any new cassette can be mixed with any previously generated cassette to allow rapid generation of a polymer of any desired size. For example, if a polymer of size 20 is

desired, the 16mer is generated geometrically, and ligating the 16mer to the tetramer generates the 20mer in a total of only 5 ligations.

Subsequent ligation to 5'- and 3'-terminal cassettes can enable production of a functional multimer. The multimer's size, based on actual molecular weight, is approximately a whole number multiple of the original. In addition, the composition of the multimer is almost identical to the monomer, differing only because of any linker sequences or terminal flanking regions that are used.

It is important to note that the polymerization does not require flanking sites. Without flanking sites, the ligations can occur with the fragments joined in either orientation, and more laborious subsequent analysis is needed to identify the correct constructs. In contrast, use of flanking sites facilitates the process by enabling oriented ligations.

4. Ligate the cassettes together to give a full length, functional, multimer.

The cassettes can be ligated sequentially as shown in **Figure 4**, or an insertion cassette can be created from the 5'- and 3'-terminal cassettes as diagramed in **Figure 5** with subsequent insertion of the polymerized amplification cassette as shown in **Figures 6, 7, and 8**. The use of an insertion cassette expedites the creation of a series of multimers with the same 5' and 3' terminal elements. **Figure 6** illustrates a technique for the ligation of the fragment from an amplification cassette into an insertion cassette using only the restriction pair restriction sites. However, the ligation is not oriented, necessitating additional analysis to identify correct constructs. **Figures 7 and 8** show equivalent oriented ligations that result from different arrangements of flanking sequences.

Figure 4 illustrates a method of making a multimer cassette from two cassettes from a multimer assembly utilizing flanking sites comprising a first cassette comprising either a 5'-restriction pair member or a 3'-restriction pair member and a second cassette comprising both a 5'-restriction pair member and a 3'-restriction pair member and further comprising:

- 1) providing the first cassette with a first flanking restriction site at one end, either 5' or 3', of its insert sequence;
- 2) providing the second cassette with a second flanking restriction site that is, or is made, ligation compatible with the first flanking site and is on the same side, either 5' or 3', of its insert sequence as the first flanking restriction site is relative to the first cassette's insert sequence;
- 3) digesting the first cassette at its restriction pair member and the first flanking site and isolating the first fragment containing the insert sequence;
- 4) digesting the second cassette at its restriction pair member partner to the first cassette's restriction pair member and at the second flanking site and isolating the second fragment containing the insert sequence;
- 5) ligating the first fragment with the second fragment to generate a multimer cassette.

The identities of the first and second cassettes can vary. For example, the first cassette can be a 3'-terminal cassette and the second cassette an amplification cassette; the first cassette can be a 5'-terminal cassette and the second cassette an amplification cassette, the first cassette can be a 3'-terminal cassette and the second cassette a multimer cassette constructed from a 5'-terminal cassette and an amplification cassette, or the first cassette can be a 5'-terminal cassette and the second cassette a multimer cassette constructed from a 3'-terminal cassette and an amplification cassette.

For the case when the first cassette is a 3'-terminal cassette and the second cassette is an amplification cassette, if the amplification cassette is digested at its 3' restriction pair member and a flanking restriction site on the 5' side of its 5' restriction member to generate a ligatable fragment, then the 3'-terminal cassette is digested at its 5' restriction pair member and a flanking restriction site on the 5' side of this member to generate a ligatable cassette. Alternatively, if the amplification cassette is digested at its 3' restriction pair member and a flanking restriction site on the 3' side of this member to generate a ligatable cassette, then the 3'-terminal cassette is digested at its 5' restriction

pair member and a flanking restriction site on the 3' side of its complete insert to generate a ligatable fragment.

It is important to note that the ligation of cassettes together does not require flanking sites. However, flanking sites enable oriented ligations. For example, if flanking sites are absent, a method of making a multimer cassette from two cassettes from a multimer assembly comprising a first cassette comprising either a 5'-restriction pair member or a 3'-restriction pair member and a second cassette comprising both a 5'-restriction pair member and a 3'-restriction pair member comprises:

- 1) digesting the first cassette at its restriction pair member and isolating the first fragment containing the insert sequence;
- 2) digesting the second cassette at both its restriction pair member sites and isolating the second fragment containing the insert sequence;
- 3) ligating the first fragment with the second fragment and screening for correct ligation orientation to generate a multimer cassette.

Again, the identities of the first and second cassettes can vary. The first cassette can be a 3'-terminal cassette and the second cassette an amplification cassette, the first cassette can be a 5'-terminal cassette and the second cassette an amplification cassette, the first cassette can be a 3'-terminal cassette and the second cassette a multimer cassette constructed from a 5'-terminal cassette and an amplification cassette, or the first cassette can be a 5'-terminal cassette and the second cassette a multimer cassette constructed from a 3'-terminal cassette and an amplification cassette.

Figure 5 illustrates a method of making an insertion cassette from the 5'-terminal cassette and the 3'-terminal cassette when each shares an insertion restriction site. The method comprises:

- 1) providing the 5'-terminal cassette with a first flanking restriction site, independent of the insertion restriction site, that is outside of the sequence including the insert sequence and insertion restriction site of the 5'-terminal cassette;

- 2) providing the 3'-terminal cassette with a second flanking restriction site, independent of the insertion restriction site, that is outside of the sequence including the insert sequence and insertion restriction site of the 3'-terminal cassette and is, or is made, ligation compatible with the first flanking site and is on the same side, either 5' or 3', of its insert sequence as the first flanking restriction site is relative to the 5'-terminal cassette's insert sequence;
- 3) digesting the 5'-terminal cassette at its insertion restriction site and the first flanking site and isolating the first fragment containing the insert sequence;
- 4) digesting the 3'-terminal cassette at its insertion restriction site and the second flanking site and isolating the second fragment containing the insert sequence;
- 5) ligating the first fragment with the second fragment to generate an insertion cassette.

Figure 6 illustrates a method of making a multimer cassette comprising an insertion cassette and an amplification cassette from a multimer assembly comprising:

- 1) digesting the insertion cassette at both its restriction pair member sites and isolating the first fragment containing the insert sequence;
- 2) digesting the amplification cassette at both its restriction pair member sites and isolating the second fragment containing the insert sequence;
- 3) ligating the first fragment with the second fragment and screening for correct ligation orientation to generate a multimer cassette.

Figures 7 and 8 illustrate a method of making a multimer cassette comprising an insertion cassette and an amplification cassette comprising:

- 1) digesting the amplification cassette at the insertion restriction site and its restriction pair member on the opposite side, either 5' or 3', of the

insert sequence and isolating the first fragment containing the insert sequence;

2) digesting the insertion cassette at the insertion restriction site and the restriction pair member partner to the digested amplification cassette's restriction pair member and isolating the second fragment containing the insert sequence;

3) ligating the first fragment with the second fragment to generate a multimer cassette precursor;

4) digesting the multimer cassette precursor at both restriction pair members, isolating the fragment containing the insert sequence, and ligating it with itself to generate a multimer cassette.

Once constructed, the gene for the multimer can be used as an insert to construct other cassettes or to express it in a suitable transcription and translation system. Once isolated in the correct conformation and with the necessary degree of purity, polymeric polypeptides are available for applications in the fields of medicine, veterinary care, research and development, diagnostics, etc. The present invention comprises proteins made from multimer assemblies of the present invention.

Each cassette can involve a fusion of any of a number of functional elements. For example, any construction involving a linker is by nature a heteromultimer, because the monomer contains at least two functional elements. A particularly expeditious method to produce these fusions is to treat each functional element as a nested assembly. In other words, each element itself is an assembly that consists of individual cassettes.

The current methods are easily extended to heteromultimers if two sequences share compatible restriction sites. For instance, two distinct monomer amplification cassettes, A and B, can be ligated together if they share the same restriction pair. Subsequent polymerization of this new "monomer" results in an alternating sequence, ABAB... Any pattern of alternating sequences can theoretically be constructed from any number of initial monomers. For example, the pattern ABBCABBC... is just one possibility.

II MULTIMER ASSEMBLIES AND MULTIMER CASSETTES

The present invention includes multimer assemblies made using the methods of the present invention and novel cassettes incorporating novel restriction pair members. In some preferred aspects of the present invention, a multimer assembly of the present invention comprises two or more amplification cassettes, in which fused 5' and 3' restriction pair member sites join the amplification cassettes. An amplification cassette can comprise any practical number of monomer sequences.

Multimer assemblies of the present invention comprise component constructs having 5' restriction pair members, 3' restriction pair members, or both 5' restriction pair members and 3' restriction pair members that can be used to make multimer cassettes, including multimer expression cassettes. Such cassettes are synthesized by joining component cassettes (such as 5'-terminal cassettes, 3'-terminal cassettes, and amplification cassettes) by ligating a 3' restriction pair member site of one component cassette to a 5' restriction pair member site of another component cassette.

One multimer assembly of the present invention comprises one or more amplification cassettes and at least one 3'-terminal cassette. Another multimer assembly of the present invention comprises one or more amplification cassettes and at least one 5'-terminal cassette. Another multimer assembly of the invention comprises one or more amplification cassettes, at least one 3'-terminal cassette, and at least one 5'-terminal cassette.

Multimer expression cassettes made from multimer assemblies of the present invention include, for example, multimer cassettes in which a 5'-terminal cassette is fused to an amplification cassette comprising a single monomer, multimer cassettes in which a 5'-terminal cassette is fused to a multimer amplification cassette constructed from multiple amplification cassettes, and multimer cassettes in which a 5'-terminal cassette is fused to a multimer cassette comprising one or more amplification cassettes and at least one 3'-terminal cassette. Multimer expression cassettes made from multimer assemblies of the present invention also include, for example, multimer cassettes in which a 3'-terminal cassette is fused to an amplification cassette, multimer cassettes in which a 3'-terminal cassette is fused to a multimer amplification cassette constructed

from multiple amplification cassettes, and multimer cassettes in which a 3'-terminal cassette is fused to a multimer cassette comprising one or more amplification cassettes and at least one 5'-terminal cassette.

The present invention also includes novel amplification cassettes. In one aspect of the present invention, an amplification cassette comprises at least one linker, in which at least one of the one or more linkers comprises at least one restriction pair partner.

Amplification cassettes can be fused using restriction pair partners, at least one of which is introduced in the linker, to form a multimer amplification cassette. The method of making the multimer amplification cassette is by joining two or more amplification cassettes by ligating the first restriction pair partner of at least one of the two or more amplification cassettes to the second restriction pair partner of at least one other of the two or more amplification cassettes to generate a multimer cassette. The present invention includes multimer amplification cassettes comprising component amplification cassettes that incorporate linkers, and multimer assemblies and multimer expression cassettes that include such multimer amplification cassettes.

Also included as amplification cassettes of the present invention are amplification cassettes that comprise monomer sequences in noncontiguous orientation. For example, an amplification cassette can comprise a 5' segment of a monomer sequence and a 3' segment of a monomer sequence that together comprise the sequence of a complete monomer, in which the 5' segment is positioned 3' of the 3' monomer segment. In these embodiments, the 5' terminus of the 3' monomer segment is preferably a 5' restriction pair member and the 3' terminus of the 5' monomer segment is preferably a 3' restriction pair member. The present invention also includes multimer amplification cassettes comprising two or more amplification cassettes that comprise monomer sequence in noncontiguous orientation. Such multimer cassettes comprising multiple amplification cassettes can be made by ligating a 3' restriction member of at least one of the two or more amplification cassettes to a 5' restriction member of at least one other of the two or more amplification cassettes. The present invention also includes multimer assemblies and multimer expression cassettes that include such amplification and multimer amplification cassettes.

In yet another aspect, the present invention includes amplification cassettes that comprise 3' and 5' restriction pair members comprising restriction sites that are initially ligation incompatible but are blunt ended to make them ligation compatible. The present invention also includes multimer amplification cassettes comprising two or more
5 amplification cassettes that comprise noncompatible sites that have been blunt-ended and then ligated to join the two or more amplification cassettes. The present invention also includes multimer assemblies and multimer expression cassettes that include such amplification and multimer amplification cassettes.

10 The invention includes multimer assembly cassettes in vectors, including cloning and expression vectors, where expression vectors can be designed for *in vitro* or *in vivo* expression. The vectors can be designed for *in vivo* expression in prokaryotes or eukaryotes, including but not limited to, bacterial cells, fungal cells, algal cells, plant cells, insect cells, avian cells, and mammalian cells. The present invention also
15 encompasses cells that include such vectors and polymeric proteins made using vectors that comprise multimeric expression vectors of the present invention. The present invention also encompasses polymeric proteins expressed from the multimeric assemblies of the present invention.

The disclosed invention also encompasses the construction of different multimer
20 assemblies involving multimeric hGH, and multimer cassettes made using the methods of the present invention that comprise multimerized hGH sequences or multimerized portions of hGH. Sequences encoding hGH or portions thereof that are part of multimer cassettes and multimer assemblies of the present invention include sequences that encode hGH taking into account the redundancy of the genetic code. Sequences encoding hGH or
25 portions thereof that are part of multimer cassettes and multimer assemblies of the present invention include sequences that encode hGH can also comprise sequence changes with respect to the human GH gene sequence that change the amino acid sequence where such changes do not detrimentally affect the activity of the protein or portion thereof.

30 The hGH assemblies can differ in the functional elements included, such as those provided by 3'- or 5'-terminal elements. The ease of producing these assemblies, and the

resulting multimers and polymers, demonstrates the utility of the methods disclosed. In the examples below, restriction sites outside, and flanking, the restriction pair sites are engineered in order to facilitate the manipulation of the cassettes.

Endogenous hGH appears in several forms *in vivo* as a result of expression from more than one gene, as well as alternative gene splicing. The predominant mature form of hGH is a single polypeptide chain consisting of 191 amino acids. The DNA and protein sequences for this predominant form are given as SEQ ID NO: 1 and SEQ ID NO: 2, respectively.

In the following paragraphs, the term “engineer” refers to using standard techniques of molecular biology generally known to those skilled in the art. Standard techniques include, but are not restricted to, restriction digestion and ligation, PCR amplification and mutagenesis, DNA synthesis, DNA isolation and purification, etc., as described in Sambrook et al. (2000), which are hereby incorporated by reference. As such, the details are only described if they bear directly on the present invention or deviate from common practice.

Examples

A drawback to rhGH therapy is the need for once daily injections. Understandably, patient preference is for a minimum of injections. In an attempt to overcome this, rhGH has been formulated with PLGA in microspheres, chemically linked to PEG, and fused to HSA in order to produce longer acting versions. Here we describe the construction of families of multimeric rhGHs, according to the steps below using the general procedures shown in **Figures 1 to 8**.

Example 1

The first example involves isolation of the GH gene. Steps to isolate the hGH gene are summarized in **Figure 9**. hGH is highly expressed in the anterior pituitary gland. As a result, mRNA of hGH is abundantly found in lysates of human pituitary. The gene for hGH is PCR amplified from human pituitary cDNA (Human Pituitary Gland Quick-Clone™ cDNA, BD Biosciences Clontech, Palo Alto, CA, catalog #7173-

1) using SEQ ID NO: 3 as the 5' primer and SEQ ID NO: 4 as the 3' primer. The 5' primer has an NdeI restriction enzyme site coding for an N-terminal methionine, and the 3' primer has a BamHI restriction enzyme site immediately after the TAG stop codon. The resulting PCR fragment is isolated from the reaction mix using standard techniques, as are all subsequent ones.

The purified PCR fragment is ligated into parent plasmid pET41a (Novagen, Madison, WI) after both insert and plasmid are digested with NdeI and BamHI and purified, again using standard techniques. This plasmid ligation mixture, and all others unless otherwise indicated, is transformed into DH5 α cells and plated on LB/antibiotic plates. Single colonies are sub-cultured and plasmid DNA is isolated from each. Restriction enzyme analysis is used to confirm the presence of an insert into the plasmid, and plasmids with insert are sent for DNA sequencing using SEQ ID NO: 5 and SEQ ID NO: 6 (Novagen, Madison, WI) as amplification primers for the 5' and 3' ends, respectively. Plasmid with correct insert is identified as p0A0, and the DNA coding region and corresponding open reading frame (ORF) translation are listed in SEQ ID NO: 7 and SEQ ID NO: 8, respectively. The convention for the sequences is that the restriction sites are included at the termini of DNA sequences and only translated amino acids that eventually appear in an expressed insert are given. Expression of protein from p0A0 yields a 192 amino acid protein consisting of full length hGH with an additional N-terminal methionine.

It is convenient to engineer a high copy number plasmid that contains the hGH gene and enables digestion of the hGH gene in its interior so that 5' or 3' elements can be swapped in and out. The gene for hGH contains a convenient PstI site, CTGCAG. The plasmid p04 (SEQ ID NO: 9), a derivative of pUC19 (New England Biolabs) containing the same multi-cloning site as pET41a, is first readied by digesting with PstI, followed by Mung Bean Nuclease, and subsequent re-ligation to destroy the internal PstI site to create p04A1. Finally, the NdeI/BamHI hGH fragment from p0A0 is ligated into similarly digested p04A1 to yield p0A03.

Several examples are now given to generate assemblies for GH multimers with different linkers. Variation in the linker sequence, as well as the degree of monomer

polymerization, may alter the polymers ease of production, conformation, *in vitro* activity, *in vivo* activity, immunogenicity, etc.

Example 2

- 5 The second example involves generation of an assembly for the direct fusion multimer of GH.

There is not a convenient restriction pair at the termini of rhGH, so this example uses the methods for a monomer sequence with an internal restriction pair. A direct fusion assembly for hGH is constructed with the features diagrammed in **Figure 2**.

- 10 Disclosed are two 5'-terminal cassettes, the amplification cassettes, and two 3'-terminal cassettes. The 3'-terminal cassette is engineered to enable construction of an insertion cassette, as shown in **Figure 5**. This facilitates insertion of amplification cassettes to generate expressible genes for different size homopolymeric GHs.

- Two 5'-terminal cassettes for the GH fusion protein assembly are disclosed. The
15 first is a direct start 5'-terminal cassette, and the second is an OmpA start 5'-terminal cassette. The direct start results in an N-terminal methionine at the N-terminus of the final expressed GH polymer. Its construction is straight forward because the insert in p0A0 and p0A03 already has the N-terminal methionine fused to the GH gene. In contrast, the OmpA start codes for an N-terminal leader sequence that targets the polymer
20 to the periplasmic space of *E. coli*, resulting in the cleavage of the leader from the polymer. There are many other 5'-terminal cassettes that can easily be generated by those skilled in the art.

- A pre- 5'-terminal cassette is disclosed that enables fusion of the OmpA sequence to any other blunt end or HindIII digested sequence. SEQ ID NO: 10 is a synthetic DNA
25 fragment that contains the coding sequence for the OmpA leader peptide, and its ORF translation is listed in SEQ ID NO: 11. The fragment has a 5' NdeI site, the OmpA leader coding region, a 3' HindIII site for HindIII ligation or blunt end ligation after filling in the HindIII 5' overhang with T4 DNA polymerase, and a BamHI site for cloning flexibility. Plasmid p04 is readied by digestion to destroy an internal site, this
30 time the HindIII site. The plasmid is digested with HindIII, followed by Mung Bean Nuclease, and subsequently ligated back together to create p04A2. Both p04A2 and

insert DNA are digested with NdeI and BamHI and ligated together to yield the plasmid p0C0A2 as shown in **Figure 9**.

For the current use, a GH sequence is needed that contains a 5' blunt end or HindIII site, along with a 3' restriction site that is the 3' member of a restriction pair.

- 5 The 5' terminus is engineered with a HindIII site. Digestion with Mung Bean Nuclease after digestion with HindIII results in a blunt 5' end that leaves the 5'-terminal codon of GH, TTC, intact. Although the blunt end is not needed for the current example, in general it is necessary for ligation to other hypothetical cassettes.

- 10 There are several choices for the restriction site pair, and we choose to use GH amino acids 187 and 188, glycine and serine, that are compatible with, among other enzymes, BamHI and BclI. The two enzymes recognize sequences GGATCC and TGATCA, respectively. BamHI is assigned as the 3' member, and BclI is assigned as the 5' member.

- 15 The desired DNA sequence is generated by PCR using p0A03 as template, as shown in **Figure 10**. The 5' and 3' primers are listed in SEQ ID NO: 12 and SEQ ID NO: 13, respectively, and the DNA coding region for the insert between the 5' flanking NdeI and 3' BamHI sites is listed in SEQ ID NO: 14. The fragment is digested with HindIII and BamHI and inserted into similarly digested p04B1 to yield p0A01. Plasmid p04B1 is prepared by destroying the HindIII site in p04A1 as described for the
20 preparation of p04A2. The result is a parent plasmid with the PstI and HindIII sites destroyed.

- The 5'-terminal cassettes are now constructed from the generated sequences as shown in **Figure 10**. The XbaI/HindIII fragment from p0C0A2 is inserted into plasmid p0A01 to generate p0A11A2. The result is the OmpA 5'-terminal cassette for the GH
25 direct fusion assembly. It contains the OmpA sequence fused directly to the 5' coding region of GH. The resulting DNA insert between NdeI and BamHI is listed in SEQ ID NO: 15, with corresponding ORF listed in SEQ ID NO: 16. The direct translation start 5'-terminal cassette is constructed by ligating fragments from existing sequences. The PstI/BamHI 5' GH fragment and plasmid backbone that results from digesting p0A03 is
30 ligated with the PstI/BamHI 3' GH fragment that results from digesting p0A01 to yield p0A11A1. The resulting DNA sequence between NdeI and BamHI, and the

corresponding ORF, for p0A11A1 are listed in SEQ ID NO: 17 and SEQ ID NO: 18, respectively.

As shown in **Figure 2**, the amplification cassette must contain several components. First, it must have both the 5' and 3' members of the restriction pair to enable polymerization. In between must be the entire continuous GH sequence. Finally, if convenient, there should be flanking restriction sites for insertion and extraction of the sequence from a plasmid backbone.

The amplification cassette for the current direct fusion of GH is generated by PCR, as shown in **Figure 11**. The 5' primer is listed in SEQ ID NO: 19. It contains an NdeI site, the 5' restriction pair member BclI, followed by the codons that together code for GH amino acids 187-191, and finally codons to anneal to the GH 5'-terminal codons. The 3' primer is one previously used and listed in SEQ ID NO: 13. The PCR template is p0A03. The resulting insert DNA sequence between NdeI and BamHI is listed in SEQ ID NO: 20, with ORF sequence listed in SEQ ID NO: 21. The DNA sequence is inserted into plasmid p04A1 to yield p0A11B.

Two simple 3'-terminal cassettes are disclosed, as shown in **Figure 12**. Both code for the 3' terminus of GH, starting at the glycine and serine codons within the BclI site, amino acids 187 and 188, and ending with the translation stop codon, TAG. The first cassette, given in SEQ ID NO: 22, is a direct translation stop. The double stranded DNA is synthesized and contains an EcoRI site flanking the 5' terminus, a BclI site to ligate to BamHI, the 3' terminus of GH, a stop codon, and a SalI site for cloning flexibility. It is inserted into p04A1 by digesting the synthetic DNA and p04A1 with EcoRI and SalI and ligating the large fragments together to yield plasmid p0A11C1. The C-terminal ORF protein sequence contributed by this cassette to subsequent GH multimer constructs is given in SEQ ID NO: 23.

The second 3'-terminal cassette, given in SEQ ID NO: 24, is a synthetic DNA fragment similar to the first, except it contains the codons for a 3 amino acid polylysine tail before the stop codon. It is analogously inserted into p04A1 to yield plasmid p0A11C2. The polylysine tail is potentially useful for chemical conjugation with other molecules. SEQ ID NO: 25 is the C-terminal ORF sequence contributed by the new insert to subsequent GH multimer constructs.

Once the basic cassettes are complete, the amplification cassette can be polymerized, the 5'-terminal and 3'-terminal cassettes can be joined to form an insertion cassette, and finally amplification cassettes can be ligated to the insertion cassette to generate expressible multimers.

5

Example 3

The polymerization of the GH direct fusion amplification cassettes is performed as shown in general in **Figure 3** and specifically in **Figure 13**. The first polymerization is formation of the dimer. Plasmid p0A11B is digested with NdeI and BclI and the
10 plasmid isolated. In a separate reaction, p0A11B is digested with NdeI/BamHI and the insert isolated. The two fragments are then ligated together to yield plasmid p0A11B2. Its insert DNA sequence is listed in SEQ ID NO: 26, and the corresponding ORF translation is listed in SEQ ID NO: 27. This process is repeated, changing the identity, and thus the size, of amplification cassettes 1 and 2 in **Figure 13** to construct polymer
15 inserts of different sizes. The size of new constructs is increased fastest if the polymerization is done geometrically, each time using the most recent construct for both cassettes 1 and 2. The size is increased by one if the monomer amplification cassette, p0A11B, is used either as cassette 1 or 2. The generalized sequences for the resulting amplification cassettes are given in SEQ ID NO: 28 and SEQ ID NO: 29 for the DNA
20 and protein, respectively.

Example 4

The cassettes for the GH direct fusion assembly are designed to enable construction of insertion cassettes to facilitate generation of a variety of expressible polymers. The
25 general procedures are shown in **Figures 5** and **7** and the specifics in **Figure 14**. Different insertion cassettes can be generated with the various 5'-terminal and 3'-terminal cassettes. However, only the one involving p0A11A1 and p0A11C1 is described here. Others are constructed in exactly the same way.

Plasmid p0A11A1 is digested with EcoRI and SalI and the opened plasmid is
30 isolated. Plasmid p0A11C1 is digested with the same enzyme pair and the insert isolated. The two fragments are ligated together to generate the insertion cassette, p0A11D, and

the resulting DNA sequence is listed in SEQ ID NO: 30. Plasmid p0A11D is compatible with ligation of any of the amplification cassettes for this assembly. It need be prepared only once for all subsequent ligations, as long as the supply is sufficient.

5

Example 5

Either of the two schemes shown in **Figures 6 and 7** can be used to ligate amplification cassettes into the insertion cassette. The example given here utilizes the oriented ligation shown in **Figure 7** and subsequent digestion and re-ligation to generate final products as shown in **Figure 14**.

10

Plasmid p0A11D is digested with BamHI and EcoRI, and the plasmid is isolated. An amplification cassette is digested with BclI and EcoRI and the insert isolated. Ligation of the two fragments yields an intermediate that is converted to the multimer expression cassette after digestion with BamHI and BclI, purification, and subsequent re-ligation. The result is an expression ready insert for the direct fusion growth hormone multimer. When performed with the Nmer amplification cassette, the result is an N+1 multimer expression cassette. The insert has general DNA sequence listed in SEQ ID NO: 31 and corresponding ORF translation listed in SEQ ID NO: 32. The production of different size multimers is controlled by the size of the ligated amplification cassette.

15

20

Protein expression is achieved by digesting and ligating the multimer expression cassette insert into an appropriate expression system. For example, the insert can be liberated with NdeI and SalI and ligated into similarly digested pET41a, followed by transformation into *E. coli* strain BL21(DE3) (Novagen).

25

One utility of the invention is the ease of production of different size multimers and different variations once the basic cassettes, p0A11A1, p0A11A2, p0A11B, p0A11C1, and p0A11C2, for example, are constructed. Those skilled in the art can easily see how substituting p0A11C2 for p0A11C1 when generating the insertion cassette generates a polylysine tail variant.

Example 6

30

The next example involves generation of a GH multimer with a linker without a convenient restriction pair. The one amino acid linker, glycine, is used as an example.

The construction of GH multimers with a glycine linker is analogous to the construction of the fusion protein. In fact, the GH glycine linker assembly shares the same 5'- and 3'-terminal cassettes with the GH fusion protein assembly. This is one advantage of the assembly construction scheme given in **Figure 2**. Assemblies differing only in the linker region only need different amplification cassettes, while sharing the same 5'- and 3'-terminal cassettes.

Use p0A11A1 and p0A11A2 as before for the direct start and OmpA 5'-terminal cassettes for the direct fusion assembly. Use p0A11C1 and p0A11C2 as before for direct stop and poly lysine 3'-terminal cassettes.

The only difference is the amplification cassettes that contain a glycine codon between the ending and starting codons for GH. The glycine linker amplification cassette is made in the same way as the one for the direct fusion homomultimer except for some necessary substitutions of sequences, as shown in **Figure 15**. SEQ ID NO: 33 is substituted for SEQ ID NO: 19 as the 5' PCR primer. It contains the same elements as before, as well as the glycine codon between the sequence for amino acids 191 and 1. The resulting PCR fragment is inserted into parent plasmid p04A1 by digesting both the parent plasmid and the PCR fragment with NdeI and BamHI and ligating the appropriate fragments together. The resulting plasmid is labeled p0A21B. The DNA sequence and ORF translation for the insert sequence between NdeI and BamHI are listed in SEQ ID NO: 34 and SEQ ID NO: 35, respectively.

The construction of additional amplification assemblies, the insertion cassette, and multimer expression cassettes for the GH glycine linker assembly is identical in practice to the one for the GH direct fusion assembly, **Figures 13 and 14**, except for the substitution of p0A21B for p0A11B. The corresponding generalized amplification cassette insert DNA and ORF sequences are listed in SEQ ID NO: 36 and SEQ ID NO: 37, and the general formulas for the multimer expression cassettes are listed in SEQ ID NO: 38 and SEQ ID NO: 39.

The previous examples have demonstrated, among other things, the ease at which multiple 5'- and 3'-terminal cassettes can be used to introduce variations in the N- and C-termini of a polymer. In the case of the 5'-terminal cassettes, cassettes with either a direct translation start or one introducing a leader sequence are disclosed. In the case of

the 3'-terminal cassettes, ones with either a direct stop or one introducing a polylysine tail are disclosed. Each demonstrates the ease at which functional elements can be added to the beginning or end of a polymer sequence. These methods are easily extended to other examples by those skilled in the art. Therefore, subsequent examples will be

5 limited to the presentation of only a single 5'- and 3'-terminal cassette for each assembly.

The next examples involve generation of GH multimers utilizing linkers that result in monomers with a terminal restriction pair. **Figure 1** details the general features for these assemblies.

10 Example 7

This example involves a linker that is noteworthy because it contains a 3' restriction pair member with a functional stop codon that is destroyed upon polymerization. Use of this linker makes it possible to express functional multimers using just the 5'-terminal and amplification cassettes. However, a 3'-terminal cassette is
15 necessary to express homomultimers without any residual linker at the 3' terminus of the protein.

The 5' restriction pair member is NcoI, C[^]CATGG, while the 3' restriction pair member is RcaI, T[^]CATGA. Therefore, the resulting linker sequence is A-Ser-Trp-B, where A and B are arbitrary protein sequences. For the given example, A is a null
20 sequence, and B is G₄S, where the single letter amino acid abbreviations are used.

For this example, only one 5'-terminal cassette is disclosed, with a direct ATG start codon and no leader sequence, as shown in **Figure 16**. The PCR primers for the 5'-terminal cassette are listed in SEQ ID NO: 3 and SEQ ID NO: 40, for the 5' and 3' ends, respectively. The 5' primer maintains the NdeI site and its start codon, while the 3'
25 primer introduces a stop codon within an RcaI (or BspHI) restriction site, immediately followed by a BamHI site. The template for the reaction is p0A0.

Because the RcaI restriction site also contains the codon TCA immediately 5' of the stop codon, it also introduces a C-terminal serine residue. The resulting PCR fragment is purified and ligated into pET41a in an analogous manner for the generation
30 of p0A0. The sequence verified plasmid is labeled p0A31A, and the DNA coding region, from the NdeI to the BamHI site, and the resulting ORF protein sequence are listed in

SEQ ID NO: 41 and SEQ ID NO: 42, respectively. Expression of protein from the gene for p0A31A yields a 193 amino acid protein consisting of full length hGH with an additional N-terminal methionine and C-terminal serine.

The PCR primers for the amplification cassette are listed in SEQ ID NO: 43 and
5 SEQ ID NO: 40, for the 5' and 3' ends, respectively. The 5' primer introduces an NcoI site followed by the linker region. The NcoI site is ligation compatible with the 3' RcaI site, and any such ligation destroys the TGA stop codon by altering it to a TGG codon. The resulting PCR fragment is purified and ligated into pET41a after the PCR product and plasmid are cut with NcoI and BamHI, as shown in **Figure 16**. The sequence
10 verified plasmid is labeled p0A31B, and the DNA coding region from the NcoI to the BamHI site is listed in SEQ ID NO: 44. The ORF protein sequence coded by the insert is given in SEQ ID NO: 45.

Again, for this example, only one 3'-terminal cassette is disclosed, with a direct TAG stop codon and no other 3'-specific sequences. The 3'-terminal cassette is
15 constructed using PCR with p0A0 as template and SEQ ID NO: 43 and SEQ ID NO: 4 as 5' and 3' primers, respectively. This creates a cassette with a 5' linker and a 3' stop codon immediately following the last amino acid from the parent monomer. The PCR fragment is inserted into pET41a as before and shown in **Figure 16** to create p0A31C. The resulting DNA and protein fragments between the NdeI and BamHI sites are listed in
20 SEQ ID NO: 46 and SEQ ID NO: 47, respectively.

The scheme for the polymerization of the amplification cassettes is shown in **Figure 3**. Additional care is necessary because the parent plasmid contains RcaI sites. One way to unambiguously liberate the insert sequence for polymerization is to first digest the flanking BamHI site, isolate the insert, and then digest with RcaI. The general
25 formulas for the Nmer amplification cassette are listed in SEQ ID NO: 48 and SEQ ID NO: 49 for the DNA and corresponding ORF translation, respectively.

Example 8

The ligation of the multimer assembly cassettes must be done sequentially, as
30 shown in **Figure 4**, because the arrangement of the restriction sites in the 3'-terminal cassette is like **Figure 2d**. The first ligation involves the 5'-terminal and amplification

cassettes, rather than the 3'-terminal and amplification cassettes, to take advantage of the stop codon in the 3'-restriction member to produce expression ready inserts. The specifics are shown in **Figure 17** using procedures already described. Use of the monomeric amplification cassette, p0A31B, results in the dimeric cassette, p0A31F2, with insert DNA and corresponding ORF translation listed in SEQ ID NO: 50 and SEQ ID NO: 51. The general formulas for the N+1mer produced after ligation between the Nmer amplification and the 5'-terminal cassettes are listed in SEQ ID NO: 52 and SEQ ID NO: 53. Transfer of the insert into an appropriate expression system yields expression of the N+1 GH polymer with the SWG4S linker and C-terminal S residue.

Completion of the ligation scheme shown in **Figure 17** results in an insert with an additional monomer and the natural C-terminus of GH. If the insert from p0A31F2 is ligated into p0A31C, then the trimer expression cassette p0A31E3 is generated. In general, the formulas for the insert DNA and corresponding ORF translation when the Nmer amplification cassette is used are listed in SEQ ID NO: 54 and SEQ ID NO: 55. For p0A31E3, the monomer amplification cassette is used and N=1.

Example 9

The plasmids containing the inserts generated with the ligation scheme shown in **Figure 17** are capable of expressing rhGH polymers following standard techniques (see for example, user manuals from Novagen, Madison, WI). DNA sequences listed in SEQ ID NO: 52 with N = 0, 1, 2, 4, and 8 and prepared according to Example 8 are ligated into pET41a. The resulting plasmids are separately transformed into BL21(DE3) and separately grown in Luria Broth medium and induced to express the polymer protein by adding IPTG to a concentration of 1 mM.

Following 3 hours of induction, each culture is harvested by centrifugation and treated with SDS-PAGE sample buffer. Proteins from the samples for each culture are separated according to their molecular weights on a standard SDS-PAGE gel (Invitrogen, Carlsbad, CA). The resulting gel is stained with coomassie blue stain to visualize the protein bands. Results for the monomer (SEQ ID NO: 42), dimer (N=1 in SEQ ID NO: 53), trimer (N=2 in SEQ ID NO: 53), pentamer (N=4 in SEQ ID NO: 53), and nanamer

(N=8 in SEQ ID NO: 53) are given in **Figure 18**. As the figure demonstrates, large amounts of each polymeric rhGH are produced except for the nanamer.

Example 10

5 Linkers with convenient restriction sites offer the engineering option to generate a multitude of assemblies with cassettes that can be attached to monomers using restriction/ligation techniques. The utility of this formulation lies in the breadth of assemblies that can be constructed relatively easily. This is especially apparent when the linkers themselves are treated as assemblies nested within the construction of the multimers. Once constructed, these linker assemblies and cassettes, like any other, can be reused to produce new assemblies.

10 Nested linker assemblies are constructed having a slightly different function than the multimer assemblies. They still need an amplification cassette for the polymerization of the linker. However, the other cassettes in the assembly enable attachment of the linker to either a 5' or 3' terminus, whichever is appropriate.

15 The example given here is a series of linkers, having amino acid sequence GZGS, where Z is an arbitrary sequence of arbitrary length. The series of linkers in **Table 1** below share features that enable them to be treated similarly in terms of their engineering. All but one has a Glycine at the N-terminus of the linker that can be coded by an NaeI restriction site at the 5' end for blunt end ligation of a 5'-terminal cassette to a monomer pre-cassette. For the other linker, GS, a synthetic DNA fragment must be ligated to the monomer pre-cassette without propagation within a plasmid. Each of the linkers ends in the protein sequence GS, so that the restriction pair is identical to earlier examples utilizing the BclI and BamHI sites.

Table 1

Linker protein monomer unit	5'-terminal cassette DNA sequence	Amplification cassette DNA sequence
GS	GGATCC	TGATCAGGATCC
GS	GCCGGCGGATCC	TGATCAGGCGGATCC
GGGS	GCCGGCGGCGGATCC	TGATCAGGCGGCGGATCC
GGGS	GCCGGCGGCGGCGGATCC	TGATCAGGCGGCGGCGGATCC
GZGS	GCCGGCYGGATCC	TGATCAGGCYGGATCC
	Z is an arbitrary protein sequence, and Y is its DNA coding sequence.	

5

As a single example of the engineering of the linker assembly, we construct the $(G_4S)_x$ linker, where x indicates the degree of polymerization of the monomer sequence. The assembly is engineered like any other, and it falls into the scheme shown in **Figure 1**. The specifics are shown in **Figure 19**.

10

Two synthetic DNA sequences are needed, SEQ ID NO: 56 and SEQ ID NO: 57. The first, the 5'-terminal cassette labeled as p0D11A in **Figure 19**, is the sequence enabling addition of the linker sequence to other cassettes. It is flanked by a NcoI site, and thus with an upstream NdeI site, for cloning flexibility at the 5' terminus, contains the NaeI site to create the blunt end ligation with the glycine codon at the 5' terminus, the linker sequence, and finally the BamHI site within the GS codons. Plasmid p04 is prepared by digestion with NgoMIV, digestion with Mung Bean Nuclease, and finally re-ligation to destroy the internal NaeI site, creating plasmid p04A3. This altered plasmid, along with the insert, is digested with NcoI and BamHI and the appropriate fragments are ligated together. The resulting plasmid is labeled p0D11A. The open reading frame translation between the cleaved NaeI and the entire BamHI sites is G_4S .

20

SEQ ID NO: 57 is the sequence for the amplification cassette to create multimers of the G₄S linker. It is flanked by an NcoI site, again for cloning flexibility. It has the 5' BclI site from the restriction pair, followed by the G₄S coding sequence that ends with the BamHI site. It is inserted into p04 by cutting both plasmid and insert with NcoI and BamHI and ligating the appropriate fragments together, as shown in **Figure 19**. The resulting plasmid is labeled p0D11B.

Amplification cassette p0D11B is polymerized by the scheme shown in **Figure 3**, left hand side, to create a dimer. In this instance the decision to follow the left hand side scheme results in larger fragments that are easier to isolate. Plasmid p0D11B is digested with NdeI and BclI and the large fragment is isolated. Separately, the same parent plasmid is digested with NdeI and BamHI, this time isolating the small fragment. The two isolated fragments are then ligated together, destroying the internal BclI and BamHI sites, but preserving the flanking ones. The resulting plasmid is labeled p0D11B2, the DNA insert is listed in SEQ ID NO: 58, and the ORF translation is listed in SEQ ID NO: 59. The sequence codes for the dimer (G₄S)₂. The process can be repeated with different starting cassettes to generate any (G₄S)_x linker. In this manner, (G₄S)₄ can be generated by digesting p0D12B with NdeI and BclI and saving the large fragment and ligating in the small fragment generated by digesting it with NdeI and BamHI.

The engineering of the G₄S assembly enables the construction of a GH multimer assembly with the (G₄S)₃ linker. The (G₄S)₃ 5'-terminal cassette for ligation to the GH sequences is generated following the general scheme shown in **Figure 4**. Plasmid p0D11B2 is digested with NdeI and BclI, and the large fragment is isolated. The small fragment resulting from digestion of p0D11A with NdeI and BamHI is ligated in, creating plasmid p0D13A. The DNA and ORF sequences for the insert are listed in SEQ ID NO: 60 and SEQ ID NO: 61, respectively. The insert in p0D13A enables ligation of the (G₄S)₃ linker to the 3' end of any sequence ending in a blunt end.

Example 11

Engineering of the GH (G₄S)₃ assembly requires two new ends to the GH gene. The BclI 5' restriction pair member is needed on the 5' terminus of the amplification and 3'-terminal cassettes, and a blunt end immediately after the last codon of GH is needed

on the 3' terminus of the 5'-terminal and amplification cassettes for ligation of the (G₄S)₃ linker. There are many ways to get a blunt end at the 3' terminus of GH. Disclosed here is the use of an NcoI site that is made blunt after digestion with Mung Bean Nuclease. In addition, it is convenient to introduce a stop codon flanked by the SalI restriction site at the 3' terminus of the GH gene for construction of an insertion cassette, as shown in general in **Figure 5**.

Three new primers are used to generate the new termini on two new GH inserts by PCR using P0A03 as template, as shown in **Figure 20**. The 5' primer is listed in SEQ ID NO: 62. It contains a flanking NdeI site, the BclI 5' restriction pair member, and sequence complementary to the GH 5' terminus. It is used for both PCR reactions. The 3' primers are listed in SEQ ID NO: 63 and SEQ ID NO: 64. Both contain sequence complementary to the 3' terminus of GH. The first codes for the NcoI site at the 3' terminus for creation of a blunt end after the last GH base pair and a flanking EcoRI site, while the second introduces a stop codon followed by a SalI restriction site.

The PCR fragments are ligated into plasmid backbones as shown in **Figure 20**. The PCR fragment resulting from use of the primers listed in SEQ ID NO: 62 and SEQ ID NO: 63 is digested with NdeI and EcoRI and ligated into similarly digested p04A1 to yield p0A04, while the fragment resulting from use of the primers listed in SEQ ID NO: 62 and SEQ ID NO: 64 is digested with BclI and SalI and ligated into similarly digested p0A11C1 to give p0A41C. The insert in p0A04 between the BclI and blunt ended NcoI sites has the DNA sequence listed in SEQ ID NO: 65 and corresponding ORF translation listed in SEQ ID NO: 66. Likewise, the insert in p0A41C, the 3'-terminal cassette, between the BclI and SalI sites has the DNA sequence listed in SEQ ID NO: 67 and ORF translation listed in SEQ ID NO: 68.

The amplification cassette is generated first by ligating the (G₄S)₃ linker from plasmid p0D13A with the insert in p0A04, as shown in **Figure 21**. Plasmid p0D13A is digested with NaeI and HindIII, and the small fragment is isolated. It is ligated into p0A04 after digestion first with NcoI, then Mung Bean Nuclease, and finally HindIII to yield p0A43B. The resulting DNA sequence for the amplification cassette between the BclI and BamHI sites is listed in SEQ ID NO: 69, with corresponding ORF translation in SEQ ID NO: 70.

The direct start 5'-terminal cassette is generated by combining the 5' elements from p0A11A1 with the 3' elements from p0A43B, as shown in **Figure 21**. The small fragment resulting from digesting p0A43B with PstI and EcoRI is isolated. It is ligated to the large fragment resulting from digestion of p0A11A1 with the same enzymes to yield p0A43A. The DNA sequence for the insert between NdeI and BamHI is listed in SEQ ID NO: 71, with corresponding ORF translation in SEQ ID NO: 72.

The polymerization of the amplification cassettes again follows the scheme in **Figure 3**. The general formulas for the insert DNA and corresponding ORF translation for the Nmer amplification cassette are listed in SEQ ID NO: 73 and SEQ ID NO: 74.

The ligation of the cassettes for the GH (G₄S)₃ linker assembly to create a multimer expression cassette follows the previously described scheme shown in **Figure 7** and demonstrated in Example 4. The insertion cassette is first generated with the 5'- and 3'-terminal cassettes using EcoRI and SalI digestions. An amplification cassette insert is first isolated after digestion with BclI and EcoRI and then spliced into the insertion cassette after digestion using BamHI and EcoRI. The resultant construct is subsequently digested with BamHI and BclI and re-ligated. The resulting N+2 multimer expression cassette, where N is the degree of polymerization of the amplification cassette used, has DNA and corresponding ORF translation sequences listed in SEQ ID NO: 75 and SEQ ID NO: 76. Transfer of the insert into a suitable expression system yields multimeric GH with (G₄S)₃ linker.

Example 12

The last example is an alternative construction for a GH direct fusion assembly. It involves the use of an incompatible restriction pair that is blunt ended for ligation. Construction of this new assembly is done by ligating together fragments from earlier cassettes, since they already contain the needed elements. The construction scheme is shown in **Figure 22**.

The 5'-terminal cassette is labeled p0A51A. It is generated by combining elements from p0A11A1 and p0A04. Plasmid p0A11A1 is digested with PstI and EcoRI and the open plasmid isolated. This is ligated with the insert isolated after digesting

p0A04 with the same enzymes. The result, p0A51A, has DNA and corresponding ORF translation listed in SEQ ID NO: 77 and SEQ ID NO: 78.

The amplification and 3'-terminal cassettes are constructed in exactly the same manner as the 5'-terminal cassette, except for substituting which plasmids are digested.

5 For the amplification cassette, plasmid p0A01 is ligated with the insert from p0A04. The insert DNA and corresponding ORF sequences are listed in SEQ ID NO: 79 and SEQ ID NO: 80. Likewise, for the 3'-terminal cassette, plasmid p0A01 is ligated with the insert from p0A03. Its insert DNA and corresponding ORF translation are listed in SEQ ID NO: 81 and SEQ ID NO: 82.

10 The polymerization of amplification cassettes still follows the scheme in **Figure 3**. However, digestion at a restriction pair member now requires the additional blunt ending of its overhang. **Figure 23** shows the specifics for the current assembly. The digestions of the cassette are done sequentially so that the restriction pair is blunt ended, but the flanking restriction sites are left intact. The general formulas for the amplification
15 cassettes are listed in SEQ ID NO: 83 and SEQ ID NO: 84.

The ligation of the multimer assembly cassettes is done sequentially as shown in **Figure 4**. The digestion of any plasmid is performed as described above with blunt ending of the restriction pair member first. The general formulas for the resulting multimer expression cassette insert, using the Nmer amplification cassette, are listed in
20 SEQ ID NO: 85 and SEQ ID NO: 86.

In practice, ligations of cassettes from this assembly involves more steps, but the technique's almost universal applicability may make it the method of choice in some instances. For the current case, the assembly given in Examples 1-4 is easier to manipulate.

25

* * * * *

Those skilled in the art will recognize many equivalents to the examples presented herein, using different monomers, linkers, restriction pairs, flanking restriction sites, 5' specific sequences, 3' specific sequences, and ligation strategies. For example, the methods are flexible as to the order of ligating 5'-terminal cassettes, 3'-terminal cassettes, and amplification cassettes, and in ligating amplification cassettes to one another to form higher order amplification cassettes. Combining elements of the following claims presented here and in the description, including the examples, is within the scope of the invention and are encompassed in the following claims.

All references cited herein, including the bibliography, are incorporated by reference in their entireties.

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SEQUENCE LISTING

5 <110> Gentide Biopharmaceuticals, Inc.

Bussell, Stuart

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SEQUENCES AS DIRECT FUSIONS OR WITH LINKERS

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 gctatgctcc gcgcccacg tctgcaccag ctggcctttg acacctacca ggagtttgaa
 120

45 gaagcctata tcccaaagga acagaagtat tcattcctgc agaaccceca gacctccctc
 180

50 tgtttctcag agtctattcc gacaccctcc aacagggagg aaacacaaca gaaatccaac
 240
 ctagagctgc tccgcatctc cctgctgctc atccagtcgt ggctggagcc cgtgcagttc
 300

55 ctcaggagtg tcttcgcaa cagcctggtg tacggcgctt ctgacagcaa cgtctatgac
 360

ctcctaaagg acctagagga aggcattcaa acgctgatgg ggaggctgga agatggcagc
420

5 ccccggaactg ggcagatctt caagcagacc tacagcaagt tcgacacaaa ctcacacaac
480

gatgacgcac tactcaagaa ctacgggctg ctctactgct tcaggaagga catggacaag
540

10 gtcgagacat tcctgcgcat cgtgcagtgc cgctctgtgg agggatcatg tggcttcttc
600

ccaaccattc cttatccag gctttttgac aacgctatgc tccgcgcca tcgtctgcac
660

15 cagctggcct ttgacaccta ccaggagttt gaagaagcct atatccaaa ggaacagaag
720

20 tattcattcc tgcagaacct ccagacctcc ctctgtttct cagagtctat tccgacacct
780

tccaacaggg aggaacaca acagaaatcc aacctagagc tgctccgcat ctccctgctg
840

25 ctcattccagt cgtggctgga gcccgctgag ttctcagga gtgtcttcgc caacagcctg
900

gtgtacggcg cctctgacag caacgtctat gacctcctaa aggacctaga ggaaggcatc
960

30 caaacgctga tggggaggct ggaagatggc agcccccgga ctgggcagat cttcaagcag
1020

35 acctacagca agttcgacac aaactcacac aacgatgacg cactactcaa gaactacggg
1080

ctgctctact gttcaggaa ggacatggac aaggctcgaga cattcctgcg catcgctgag
1140

40 tgccgctctg tggagggatc c
1161

45 <210> 27

<211> 382

<212> PRT

50 <213> Artificial

55 <220>

<223> synthetic sequence

<400> 27

5	Ser Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn	1 5 10 15
	Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr	20 25 30
10	Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe	35 40 45
	Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr	50 55 60
15	Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu	65 70 75 80
	Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe	85 90 95
20	Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser	100 105 110
	Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu	115 120 125
	Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys	130 135 140
30	Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu	145 150 155 160
	Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys	165 170 175
35	Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser	180 185 190
	Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala	195 200 205
	Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln	210 215 220
45	Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu	225 230 235 240
	Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro	245 250 255
50	Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg	260 265 270
	Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu	275 280 285

Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn
 290 295 300
 Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met
 5 305 310 315 320
 Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln
 325 330 335
 10 Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu
 340 345 350
 Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val
 355 360 365
 15 Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly
 370 375 380
 <210> 28
 20 <211> 1152
 <212> DNA
 25 <213> Artificial
 <220>
 30 <223> synthetic sequence
 <220>
 35 <221> misc_feature
 <222> (574)..(1146)
 <223> sequence is repeated N-1 times, where N is a positive whole
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 <400> 28
 45 tgatcatgtg gcttcttccc aaccattccc ttatccaggc tttttgacaa cgctatgctc
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 cgcgcccatc gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat
 50 120
 atcccaaagg aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca
 180
 55 gagtctattc cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg
 240

ctccgcatct cctgctgct catccagtcg tggctggagc cctgacagt cctcaggagt
300

5 gtcttcgcca acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag
360

gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact
420

10 gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca
480

ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca
540

15 ttcttgcgca tcgtgcagtg ccgctctgtg gagggatcat gtggcttctt cccaaccatt
600

20 cccttatcca ggctttttga caacgctatg ctccgcgccc atcgtctgca ccagctggcc
660

tttgacacct accaggagtt tgaagaagcc tatatcccaa aggaacagaa gtattcattc
720

25 ctgcagaacc cccagacctc cctctgtttc tcagagtcta ttccgacacc ctccaacagg
780

gaggaaacac aacagaaatc caacctagag ctgctccgca tctccctgct gtcctccag
840

30 tcgtggctgg agcccgctgca gttcctcagg agtgtcttcg ccaacagcct ggtgtacggc
900

35 gcctctgaca gcaacgtcta tgacctcta aaggacctag aggaaggcat ccaaagctg
960

atggggaggc tggaagatgg cagcccccg actgggcaga tcttcaagca gacctacagc
1020

40 aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg gctgctctac
1080

tgcttcagga aggacatgga caaggctgag acattcctgc gcacgtgca gtgccgctct
1140

45 gtggagggat cc
1152

50 <210> 29

<211> 382

<212> PRT

55 <213> Artificial

<220>

5 <223> synthetic sequence

<220>

10 <221> MISC_FEATURE

<222> (191)..(381)

<223> sequence is repeated N-1 times, where N is a positive whole
numbe

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<400> 29

20 Ser Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn
1 5 10 15

25 Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
20 25 30

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
35 40 45

30 Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
50 55 60

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
65 70 75 80

35 Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
85 90 95

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
100 105 110

40 Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
115 120 125

45 Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
130 135 140

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
145 150 155 160

50 Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
165 170 175

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
180 185 190

55 Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala

	195	200	205
	Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln		
	210	215	220
5	Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu		
	225	230	235 240
10	Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro		
		245	250 255
	Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg		
		260	265 270
15	Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu		
		275	280 285
	Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn		
		290	295 300
20	Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met		
		305	310 315 320
	Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln		
25		325	330 335
	Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu		
		340	345 350
30	Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val		
		355	360 365
	Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly		
		370	375 380
35	<210> 30		
	<211> 606		
40	<212> DNA		
	<213> Artificial		
45	<220>		
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	60		
55	cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag		
	120		

gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt
 180
 5 ccgacaccct ccaacagga ggaaacacaa cagaaatcca acctagagct gtcctcgatc
 240
 tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgcc
 300
 10 aacagcctgg tgtaaggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag
 360
 15 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc
 420
 ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag
 480
 20 aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc
 540
 atcgtgcagt gccgctctgt ggagggatcc gaattccatt gatcatgtgg cttctagtag
 600
 25 gtcgac
 606
 30 <210> 31
 <211> 1737
 <212> DNA
 35 <213> Artificial
 <220>
 <223> synthetic sequence
 <220>
 45 <221> misc_feature
 <222> (1138)..(1710)
 50 <223> sequence is repeated N-1 times, where N is a positive whole
 numbe
 55 <400> 31

catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccac
 60
 5 cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag
 120
 gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt
 180
 10 ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gtcgccatc
 240
 tccttgctgc tcattcagtc gtggctggag cccgtgcagt tctcaggag tgtcttcgcc
 300
 15 aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag
 360
 20 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc
 420
 ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag
 480
 25 aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc
 540
 atcgtgcagt gccgctctgt ggagggatca tgtggcttct tcccaacct tcccttatcc
 600
 30 aggccttttg acaacgctat gtcgccgcc catcgtctgc accagctggc ctttgacacc
 660
 taccaggagt ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac
 720
 35 cccagacct cctctgttt ctgagagtct attccgacac cctccaacag ggaggaaaca
 780
 40 caacagaaat ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg
 840
 gagcccgtgc agttcctcag gagtgtcttc gccaacagcc tgggtgtacgg cgcctctgac
 900
 45 agcaacgtct atgacctcct aaaggacct gaggaaggca tccaaacgct gatggggagg
 960
 ctggaagatg gcagcccccg gactgggcag atcttcaagc agacctacag caagttcgac
 1020
 50 acaaactcac acaacgatga cgcactactc aagaactacg ggtgctcta ctgcttcagg
 1080
 55 aaggacatgg acaaggtcga gacattcctg cgcacgtgc agtgccgctc tgtggaggga
 1140

tcatgtggct tcttcccaac cattccctta tccaggcttt ttgacaacgc tatgctccgc
 1200

5 gcccacgctc tgcaccagct ggcctttgac acctaccagg agtttgaaga agcctatatc
 1260

ccaaaggaac agaagtattc attcctgcag aacccccaga cctccctctg tttctcagag
 1320

10 tctattccga caccctccaa cagggaggaa acacaacaga aatccaacct agagctgctc
 1380

cgcatctccc tgctgctcat ccagtctgg ctggagcccg tgcagttcct caggagtgtc
 1440

15 ttgcgaaca gcctggtgta cggcgctct gacagcaacg tctatgacct cctaaaggac
 1500

ctagaggaag gcatccaaac gctgatgggg aggctggaag atggcagccc ccggactggg
 20 1560

cagatcttca agcagacct cagcaagttc gacacaaact cacacaacga tgacgcacta
 1620

25 ctcaagaact acgggctgct ctactgcttc aggaaggaca tggacaaggt cgagacattc
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 1737

30

<210> 32

<211> 574

35 <212> PRT

<213> Artificial

40

<220>

<223> synthetic sequence

45 <220>

<221> MISC_FEATURE

50 <222> (379)..(569)

<223> sequence is repeated N-1 times, where N is a positive whole
 numbe

55

<220>

<221> mat_peptide

5 <222> (1)..()

<400> 32

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Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15

15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

20

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

25

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

30

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

35

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
130 135 140

40

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
165 170 175

45

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190

Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg
195 200 205

50

Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu
210 215 220

Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
225 230 235 240

55

Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg
245 250 255

Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu
 260 265 270
 5 Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val
 275 280 285
 Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp
 290 295 300
 10 Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu
 305 310 315 320
 Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser
 15 325 330 335
 Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr
 340 345 350
 20 Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe
 355 360 365
 Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Phe
 25 370 375 380
 Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala
 385 390 395 400
 30 His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu
 405 410 415
 Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln
 420 425 430
 35 Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu
 435 440 445
 Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu
 40 450 455 460
 Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe
 465 470 475 480
 45 Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu
 485 490 495
 Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu
 500 505 510
 50 Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys
 515 520 525
 Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly
 55 530 535 540
 Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu

545

550

555

560

Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

565

570

5

<210> 33

<211> 55

10

<212> DNA

<213> Artificial

15

<220>

<223> synthetic sequence

20

<400> 33

taccatatga catgatcatg tggcttcggt ttcccaacca ttcccttatac caggc

55

25

<210> 34

<211> 591

<212> DNA

30

<213> Artificial

35

<220>

<223> synthetic sequence

<400> 34

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60

aacgctatgc tccgcgcca tegtctgcac cagctggcct ttgacaccta ccaggagttt

120

45

gaagaagcct atatcccaaa ggaacagaag tattcattcc tgcagaaccc ccagacctcc

180

ctctgtttct cagagtctat tccgacaccc tccaacaggg aggaaacaca acagaaatcc

50

240

aacctagagc tgctccgcac ctccctgctg ctcatccagt cgtggctgga gcccgctgac

300

55

ttcctcagga gtgtcttcgc caacagcctg gtgtacggcg cctctgacag caacgtctat

360

gacctcctaa aggacctaga ggaagggcatc caaacgctga tggggagggt ggaagatggc
 420
 5 agcccccgga ctgggcagat cttcaagcag acctacagca agttcgacac aaactcacac
 480
 aacgatgacg cactactcaa gaactacggg ctgctctact gcttcaggaa ggacatggac
 540
 10 aaggtcgaga cattcctgcg catcgtgcag tgccgctctg tggagggatc c
 591
 <210> 35
 15 <211> 192
 <212> PRT
 20 <213> Artificial
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 25 <223> synthetic sequence
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 Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr
 20 25 30
 35 Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser
 35 40 45
 Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro
 40 50 55 60
 Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu
 65 70 75 80
 45 Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln
 85 90 95
 Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp
 100 105 110
 50 Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr
 115 120 125
 Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe
 55 130 135 140
 Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala

145 150 155 160
 Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp
 165 170 175
 5 Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly
 180 185 190

 10 <210> 36
 <211> 1158

 15 <212> DNA
 <213> Artificial

 20 <220>
 <223> synthetic sequence

 25 <220>
 <221> misc_feature
 <222> (577)..(1152)
 30 <223> sequence is repeated N-1 times, where N is a positive whole
 numbe

 35 <400> 36
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 40 ctccgcgccc atcgtctgca ccagctggcc tttgacacct accaggagtt tgaagaagcc
 120
 tatatcccaa aggaacagaa gtattcattc ctgcagaacc ccagacctc cctctgtttc
 180
 45 tcagagtcta ttccgacacc ctccaacagg gaggaaacac aacagaaatc caacctagag
 240
 ctgctccgca tctccctgct gctcatccag tcgtggctgg agcccgtgca gttcctcagg
 50 300
 agtgtcttcg ccaacagcct ggtgtacggc gcctctgaca gcaacgtcta tgacctcta
 360
 55 aaggacctag aggaaggcat ccaaacgctg atggggaggc tggaagatgg cagcccccg
 420

actgggcaga tcttcaagca gacctacagc aagttcgaca caaactcaca caacgatgac
480

5 gcactactca agaactacgg gctgctctac tgcttcagga aggacatgga caaggtcgag
540

acattcctgc gcatcgtgca gtgccgctct gtggagggat catgtggctt cggtttccca
600

10 accattccct tatccaggct ttttgacaac gctatgctcc ggcgccatcg tctgcaccag
660

ctggcctttg acacctacca ggagtttgaa gaagcctata tcccaaagga acagaagtat
720

15 tcattcctgc agaaccceca gacctcctc tgtttctcag agtctattcc gacaccctcc
780

20 aacagggagg aaacacaaca gaaatccaac ctagagctgc tccgcctctc cctgctgctc
840

atccagtcgt ggctggagcc cgtgcagttc ctcaggagtg tcttcgcca cagcctgggtg
900

25 tacggcgct ctgacagcaa cgtctatgac ctctaaagg acctagagga aggcattcaa
960

acgtgatgg ggaggctgga agatggcagc ccccgactg ggcagatctt caagcagacc
1020

30 tacagcaagt tcgacacaaa ctacacaaac gatgacgcac tactcaagaa ctacgggctg
1080

ctctactgct tcaggaagga catggacaag gtcgagacat tcctggcgtat cgtgcagtg
1140

cgctctgtgg agggatcc
1158

40

<210> 37

<211> 384

45 <212> PRT

<213> Artificial

50

<220>

<223> synthetic sequence

55 <220>

<221> MISC_FEATURE

<222> (192)..(383)

5 <223> sequence is repeated N-1 times, where N is a positive whole numbe

10 <400> 37

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1 5 10 15
15 Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr
20 25 30
20 Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser
35 40 45
Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro
50 55 60
25 Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu
65 70 75 80
Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln
85 90 95
30 Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp
100 105 110
35 Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr
115 120 125
Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe
130 135 140
40 Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala
145 150 155 160
Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp
165 170 175
45 Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly
180 185 190
Ser Cys Gly Phe Gly Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp
195 200 205
50 Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr
210 215 220
55 Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser
225 230 235 240

Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro
 245 250 255
 5 Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu
 260 265 270
 Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln
 275 280 285
 10 Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp
 290 295 300
 Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr
 305 310 315 320
 15 Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe
 325 330 335
 20 Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala
 340 345 350
 Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp
 355 360 365
 25 Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly
 370 375 380
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 30 <211> 1743
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 40 <223> synthetic sequence
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 45 <222> (1141)..(1716)
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cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag
 120

5 gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt
 180

ccgacaccct ccaacagggg ggaaacacaa cagaaatcca acctagagct gctccgcctc
 240

10 tccctgctgc tcatccagtc gtggctggag cccgtgcagt tctcaggag tgtcttcgcc
 300

aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag
 360

15 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc
 420

20 ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag
 480

aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc
 540

25 atcgtgcagt gccgctctgt ggagggatca tgtggcttcg gtttcccaac cattccctta
 600

tccaggcttt ttgacaacgc tatgtccgc gcccatcgtc tgcaccagct ggcctttgac
 660

30 acctaccagg agtttgaaga agcctatatc ccaaaggaa acgaagtattc attcctgcag
 720

aacccccaga cctccctctg tttctcagag tctattccga caccctcaa caggaggaa
 780

acacaacaga aatccaacct agagctgctc cgcctctccc tgctgctcat ccagtcgtgg
 840

40 ctggagcccc tgcaattcct caggagtgtc ttogccaaca gcctgggtga cggcgctct
 900

gacagcaacg tctatgacct cctaaaggac ctagaggaag gcatccaaac gctgatgggg
 960

45 aggctggaag atggcagccc ccggactggg cagatcttca agcagacctc cagcaagttc
 1020

gacacaaact cacacaacga tgacgcacta ctcaagaact acgggctgct ctactgcttc
 1080

aggaaggaca tggacaaggt cgagacattc ctgcgcctcg tgcagtgcgc ctctgtggag
 1140

55 ggatcatgtg gcttcgggtt cccaaccatt cccttatcca ggctttttga caacgctatg
 1200

ctccgcgccc atcgtctgca ccagctggcc ttgacacct accaggagtt tgaagaagcc
 1260
 5 tatatcccaa aggaacagaa gtattcattc ctgcagaacc cccagacctc cctctgtttc
 1320
 tcagagtcta ttccgacacc ctccaacagg gaggaaacac aacagaaatc caacctagag
 1380
 10 ctgctccgca tctccctgct gctcatccag tcgtggctgg agcccgtgca gttcctcagg
 1440
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 1560
 20 actgggcaga tcttcaagca gacctacagc aagtctgaca caaactcaca caacgatgac
 1620
 gcactactca agaactacgg gctgctctac tgcttcagga aggacatgga caaggtcgag
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 gac
 30 1743
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15 Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

20 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

25 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

30 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

35 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
130 135 140

40 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
165 170 175

45 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190

Gly Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
195 200 205

50 Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
210 215 220

55 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
225 230 235 240

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn

	245	250	255
5	Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser 260 265 270		
	Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser 275 280 285		
10	Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr 290 295 300		
	Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg 305 310 315 320		
15	Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr 325 330 335		
	Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn 340 345 350		
20	Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr 355 360 365		
	Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe 370 375 380		
25			
	Gly Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu 385 390 395 400		
30	Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe 405 410 415		
	Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn 420 425 430		
35			
	Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn 435 440 445		
40	Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser 450 455 460		
	Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser 465 470 475 480		
45			
	Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr 485 490 495		
	Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg 500 505 510		
50			
	Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr 515 520 525		
55	Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn 530 535 540		

	Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr
	545					550					555					560

5	Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe
					565					570					575	

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10 <212> DNA

<213> Artificial

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20 <400> 40

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39

25

<210> 41

<211> 591

30 <212> DNA

<213> Artificial

35

<220>

<223> synthetic sequence

40 <400> 41

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45 cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag

120

gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt

180

50 ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gtcctcgatc

240

tcctgtctgc tcatccagtc gtggctggag cccgtgcagt tctcaggag tgtcttcgcc

55 300

aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag
 360
 5 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc
 420
 ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag
 480
 10 aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc
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 20 <212> PRT
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 35 Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 20 25 30
 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 40 35 40 45
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60
 45 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95
 50 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110
 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
 115 120 125
 55 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr

	130	135	140
	Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn		
	145	150	155 160
5	Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr		
		165	170 175
10	Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe		
		180	185 190
	Ser		
15	<210> 43		
	<211> 50		
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20	<213> Artificial		
25	<220>		
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35	<210> 44		
	<211> 606		
	<212> DNA		
40	<213> Artificial		
45	<220>		
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	60		
	atgctccgcg cccatcgtct gcaccagctg gcctttgaca cctaccagga gtttgaagaa		
	120		
55	gcctatatcc caaaggaaca gaagtattca ttctgcaga acccccagac ctccctctgt		
	180		

ttctcagagt ctattccgac accctccaac agggaggaaa cacaacagaa atccaaccta
 240

5 gagctgctcc gcattccct gctgctcatc cagtcgtggc tggagcccgt gcagttcctc
 300

aggagtgtct tcgccaacag cctgggtgtac ggcgcctctg acagcaacgt ctatgacctc
 360

10 ctaaaggacc tagaggaagg catccaaacg ctgatgggga ggctggaaga tggcagcccc
 420

cggactgggc agatcttcaa gcagacctac agcaagttcg acacaaactc acacaacgat
 480

15 gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat ggacaaggtc
 540

20 gagacattcc tgcgcatcgt gcagtgccgc tctgtggagg gcagctgtgg cttctcatga
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ggatcc
 606

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 <211> 198

30 <212> PRT
 <213> Artificial

35 <220>
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40 <400> 45

Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe
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45 Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp
 20 25 30

Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr
 35 40 45

50 Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile
 50 55 60

55 Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu
 65 70 75 80

Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val

	85	90	95
	Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser		
	100	105	110
5	Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln		
	115	120	125
	Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile		
10	130	135	140
	Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp		
	145	150	155 160
15	Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met		
	165	170	175
	Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu		
20	180	185	190
	Gly Ser Cys Gly Phe Ser		
	195		
	<210> 46		
25	<211> 603		
	<212> DNA		
30	<213> Artificial		
	<220>		
35	<223> synthetic sequence		
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	atgctccgcg cccatcgtct gcaccagctg gcctttgaca cctaccagga gtttgaagaa		
	120		
45	gcctatatcc caaaggaaca gaagtattca ttctctgcaga acccccagac ctccctctgt		
	180		
	ttctcagagt ctattccgac accctccaac agggaggaaa cacaacagaa atccaaccta		
	240		
50	gagctgctcc gcattccct gctgctcatc cagtcgtggc tggagcccgt gcagttcctc		
	300		
	aggagtgtct tcgccaacag cctgggtgtac ggcgccctctg acagcaacgt ctatgacctc		
55	360		

ctaaaggacc tagaggaagg catccaaacg ctgatgggga ggctggaaga tggcagcccc
420

5 cggactgggc agatcttcaa gcagacctac agcaagttcg acacaaactc acacaacgat
480

gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat ggacaaggtc
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10 gagacattcc tgcgcacgt gcagtgcgcg tctgtggagg gcagctgtgg cttctagggga
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tcc
603

15

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<211> 197

20 <212> PRT

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<400> 47

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35 Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp
20 25 30

Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr
40 35 40 45

Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile
50 55 60

45 Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu
65 70 75 80

Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val
85 90 95

50 Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser
100 105 110

Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln
55 115 120 125

Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile

	130	135	140
	Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp		
	145	150	155 160
5	Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met		
		165 170	175
10	Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu		
		180 185	190
	Gly Ser Cys Gly Phe		
	195		
15	<210> 48		
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	<212> DNA		
20	<213> Artificial		
25	<220>		
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30	<221> misc_feature		
	<222> (595)..(1188)		
35	<223> sequence is repeated N-1 times, where N is a positive whole numbe		
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45	atgctccgcg cccatcgtct gcaccagctg gcctttgaca cctaccagga gtttgaagaa		
	120		
	gcctatatcc caaaggaaca gaagtattca ttctgcaga acccccagac ctccctctgt		
	180		
50	ttctcagagt ctattccgac accctccaac agggaggaaa cacaacagaa atccaaccta		
	240		
	gagctgctcc gcattctcct gctgctcacc cagtcgtggc tggagcccgt gcagttcttc		
55	300		

5 aggagtgtct tcgccaacag cctgggtgtac ggcgcctctg acagcaacgt ctatgacctc
 360
 10 ctaaaggacc tagaggaagg catccaaacg ctgatgggga ggctggaaga tggcagcccc
 420
 15 cggactgggc agatcttcaa gcagacctac agcaagttcg acacaaactc acacaacgat
 480
 20 gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat ggacaaggtc
 540
 25 gagacattcc tgcgcatcgt gcagtgcgcg tctgtggagg gcagctgtgg cttctcatgg
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 30 ggtgggtggag gaagtttccc aaccattccc ttaticcaggc tttttgacaa cgctatgctc
 660
 35 cgcgcccata gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat
 720
 40 atcccāaagg aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca
 780
 45 gagtctattc cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg
 840
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 960
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 1020
 65 gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca
 1080
 70 ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca
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 85 <211> 396
 90 <212> PRT
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10 <222> (198)..(395)

<223> sequence is repeated N-1 times, where N is a positive whole
numbe

15

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Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp
20 25 30

25 Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr
35 40 45

Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile
50 55 60

30 Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu
65 70 75 80

35 Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val
85 90 95

Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser
100 105 110

40 Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln
115 120 125

Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile
130 135 140

45 Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp
145 150 155 160

50 Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met
165 170 175

Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu
180 185 190

55 Gly Ser Cys Gly Phe Ser Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile
195 200 205

Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu
 210 215 220

5 His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile
 225 230 235 240

Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu
 245 250 255

10 Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln
 260 265 270

Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln
 15 275 280 285

Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser
 290 295 300

20 Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp
 305 310 315 320

Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser
 25 325 330 335

Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr
 340 345 350

Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr
 30 355 360 365

Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val
 370 375 380

35 Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Ser
 385 390 395

<210> 50

40 <211> 1185

<212> DNA

<213> Artificial

45

<220>

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 120

gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt
 180

5 ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcatc
 240

tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgcc
 300

10 aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag
 360

15 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gcccccgac tgggcagatc
 420

ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag
 480

20 aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc
 540

atcgtgcagt gccgctctgt ggagggcagc tgtggcttct catggggtgg tggaggaagt
 600

25 ttcccaacca ttcccttata caggtttttt gacaacgcta tgctccgcgc ccatcgtctg
 660

30 caccagctgg cctttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag
 720

aagtattcat tcctgcagaa cccccagacc tccctctgtt tctcagagtc tattccgaca
 780

35 ccctccaaca gggaggaaac acaacagaaa tccaacctag agctgctccg catctccctg
 840

ctgctcatcc agtcgtggct ggagcccgct cagttcctca ggagtgtctt cgccaacagc
 900

40 ctggtgtacg gcgcctctga cagcaacgtc tatgacctcc taaaggacct agaggaaggc
 960

45 atccaaacgc tgatggggag gctggaagat ggcagcccc ggactgggca gatcttcaag
 1020

cagacctaca gcaagttcga cacaactca cacaacgatg acgcactact caagaactac
 1080

50 gggctgctct actgcttcag gaaggacatg gacaaggctg agacattcct gcgcatcgtg
 1140

cagtgccgct ctgtggaggg cagctgtggc ttctcatgag gatcc
 1185

55

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 <211> 391
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 15 <220>
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 1 5 10 15
 Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 20 25 30
 30 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 35 50 55 60
 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80
 40 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110
 45 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
 115 120 125
 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 50 130 135 140
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 145 150 155 160
 55 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
 165 170 175

	Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe	
				180					185					190			
5	Ser	Trp	Gly	Gly	Gly	Gly	Ser	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	
			195					200					205				
	Phe	Asp	Asn	Ala	Met	Leu	Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	
		210					215					220					
10	Asp	Thr	Tyr	Gln	Glu	Phe	Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	
	225					230					235					240	
	Tyr	Ser	Phe	Leu	Gln	Asn	Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	
				245					250						255		
15	Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	
				260					265					270			
	Glu	Leu	Leu	Arg	Ile	Ser	Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	
20			275				280						285				
	Val	Gln	Phe	Leu	Arg	Ser	Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	
		290					295					300					
25	Ser	Asp	Ser	Asn	Val	Tyr	Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	
	305				310						315					320	
	Gln	Thr	Leu	Met	Gly	Arg	Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	
				325						330					335		
30	Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	
			340						345					350			
	Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	
35			355					360					365				
	Met	Asp	Lys	Val	Glu	Thr	Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	
		370					375					380					
40	Glu	Gly	Ser	Cys	Gly	Phe	Ser										
	385					390											
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45	<211>	1779															
	<212>	DNA															
	<213>	Artificial															
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55	<223>	synthetic sequence															

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<221> misc_feature

5 <222> (1174)..(1767)

<223> sequence is repeated N-1 times, where N is a positive whole
numbe

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60

cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag
120

20 gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt
180

ccgacaccct ccaacagggg ggaacacaaa cagaaatcca acctagagct gctccgcac
240

25 tccttctgtc tcatccagtc gtggctggag cccgtgcagt tcttcaggag tgtcttcgcc
300

30 aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag
360

gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc
420

35 ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag
480

aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc
540

40 atcgtgcagt gccgctctgt ggagggcagc tgtggcttct catgggggtg tggaggaagt
600

45 ttcccaacca ttcccttata caggcttttt gacaacgcta tgctccgcgc ccatcgtctg
660

caccagctgg cctttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag
720

50 aagtattcat tctgcagaa cccccagacc tccctctgtt tctcagagtc tattccgaca
780

ccctccaaca gggaggaaac acaacagaaa tccaacctag agctgctccg catctccctg
840

55 ctgctcatcc agtcgtggct ggagcccgtg cagttcctca ggagtgtctt cgccaacagc
900

ctgggtgtacg gcgcctctga cagcaacgtc tatgacctcc taaaggacct agaggaaggc
960

5 atccaaacgc tgatggggag gctggaagat ggcagcccc ggactgggca gatcttcaag
1020

cagacctaca gcaagttcga cacaaactca cacaacgatg acgcactact caagaactac
1080

10 gggctgctct actgcttcag gaaggacatg gacaaggctg agacattcct gcgcacgtg
1140

cagtgcgct ctgtggaggg cagctgtggc ttctcatggg gtggtggagg aagtttccca
1200

15 accattccct tatccaggct ttttgacaac gctatgctcc gcgcccacg tctgcaccag
1260

20 ctggcctttg acacctacca ggagtttgaa gaagcctata tcccaaagga acagaagtat
1320

tcattcctgc agaaccacca gacctccctc tgtttctcag agtctattcc gacaccctcc
1380

25 aacaggagg aaacacaaca gaaatccaac ctagagctgc tccgcatctc cctgctgctc
1440

atccagtcgt ggctggagcc cgtgcagttc ctcaggagtg tcttcgcaa cagcctggtg
1500

30 tacggcgct ctgacagcaa cgtctatgac ctctaaagg acctagagga aggcattcaa
1560

35 acgctgatgg ggaggctgga agatggcagc ccccgactg ggcagatctt caagcagacc
1620

tacagcaagt tcgacacaaa ctcacacaac gatgacgcac tactcaagaa ctacgggctg
1680

40 ctctactgct tcaggaagga catggacaag gtcgagacat tctgcgcat cgtgcagtgc
1740

cgctctgtgg agggcagctg tggcttctca tgaggatcc
1779

45

<210> 53

50 <211> 589

<212> PRT

<213> Artificial

55

<220>

<223> synthetic sequence

5 <220>

<221> MISC_FEATURE

<222> (391)..(588)

10 <223> sequence is repeated N-1 times, where N is a positive whole numbe

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<221> mat_peptide

20 <222> (1)..()

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20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

40 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

45 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

50 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
130 135 140

55 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145 150 155 160

	Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr	
					165					170					175		
5	Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe	
				180					185					190			
	Ser	Trp	Gly	Gly	Gly	Gly	Ser	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	
			195					200					205				
10	Phe	Asp	Asn	Ala	Met	Leu	Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	
		210						215				220					
	Asp	Thr	Tyr	Gln	Glu	Phe	Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	
	225				230					235							240
15	Tyr	Ser	Phe	Leu	Gln	Asn	Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	
					245					250						255	
	Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	
20				260						265					270		
	Glu	Leu	Leu	Arg	Ile	Ser	Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	
			275					280					285				
25	Val	Gln	Phe	Leu	Arg	Ser	Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	
		290						295				300					
	Ser	Asp	Ser	Asn	Val	Tyr	Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	
	305				310					315							320
30	Gln	Thr	Leu	Met	Gly	Arg	Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	
					325					330						335	
	Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	
35				340					345					350			
	Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	
			355					360					365				
40	Met	Asp	Lys	Val	Glu	Thr	Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	
		370						375				380					
	Glu	Gly	Ser	Cys	Gly	Phe	Ser	Trp	Gly	Gly	Gly	Gly	Ser	Phe	Pro	Thr	
	385				390						395					400	
45	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu	Arg	Ala	His	Arg	
					405				410						415		
	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe	Glu	Glu	Ala	Tyr	
50			420					425					430				
	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn	Pro	Gln	Thr	Ser	
			435					440				445					
55	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu	Glu	Thr	
		450						455				460					

Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile
 465 470 475 480

5 Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn
 485 490 495

Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys
 500 505 510

10 Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly
 515 520 525

Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp
 530 535 540

Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu
 545 550 555 560

20 Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile
 565 570 575

Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Ser
 580 585

25 <210> 54
 <211> 2370

30 <212> DNA
 <213> Artificial

35 <220>
 <223> synthetic sequence

40 <220>
 <221> misc_feature
 <222> (1174)..(1767)

45 <223> sequence is repeated N-1 times, where N is a positive whole
 numbe

50 <400> 54
 catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgccat
 60

55 cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag
 120

gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt
 180

5 ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac
 240

tccctgctgc tcatccagtc gtggctggag cccgtgcagt tctcaggag tgtcttcgcc
 300

10 aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag
 360

15 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc
 420

ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag
 480

20 aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc
 540

atcgtgcagt gccgctctgt ggagggcagc tgtggcttct catggggtgg tggaggaagt
 600

25 ttcccaacca ttcccttctc caggcttttt gacaacgcta tgctccgcgc ccatcgtctg
 660

30 caccagctgg cctttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag
 720

aagtattcat tctgcagaa ccccagacc tccctctgtt tctcagagtc tattccgaca
 780

35 ccctccaaca gggaggaaac acaacagaaa tccaacctag agctgctccg catctccctg
 840

ctgctcacc agtcgtggct ggagcccgtg cagttcctca ggagtgtctt cgccaacagc
 900

40 ctggtgtacg ggcctctga cagcaacgct tatgacctcc taaaggacct agaggaaggc
 960

45 atccaaacgc tgatggggag gctggaagat ggcagcccc ggactgggca gatcttcaag
 1020

cagacctaca gcaagttcga cacaactca cacaacgatg acgcactact caagaactac
 1080

50 gggctgctct actgcttcag gaaggacatg gacaaggctg agacattcct gcgcacgtg
 1140

cagtgccgt ctgtggaggg cagctgtggc ttctcatggg gtggaggagg aagtttccca
 1200

55 accattccct tatccaggct ttttgacaac gctatgctcc gcgccatcg tctgcaccag
 1260

ctggcctttg acacctacca ggagtttgaa gaagcctata tcccaaagga acagaagtat
1320

5 tcattcctgc agaaccceca gacctccctc tgtttctcag agtctattcc gacaccctcc
1380

aacagggagg aacacacaac gaaatccaac ctagagctgc tccgcatctc cctgctgctc
1440

10 atccagtcgt ggctggagcc cgtgcagtgc ctcaggagtg tcttcgcctc cagcctgggtg
1500

tacggcgccct ctgacagcaa cgtctatgac ctccctaaagg acctagagga aggcattccaa
1560

15 acgctgatgg ggaggctgga agatggcagc ccccgactg ggcagatctt caagcagacc
1620

20 tacagcaagt tcgacacaaa ctcacacaaac gatgacgcac tactcaagaa ctacgggctg
1680

ctctactgct tcaggaagga catggacaag gtcgagacat tctgctgcat cgtgcagtgc
1740

25 cgctctgtgg agggcagctg tggcttctca tgggggtggg gaggaagttt cccaaccatt
1800

cccttatcca ggctttttga caacgctatg ctccgcgccc atcgtctgca ccagctggcc
1860

30 tttgacacct accaggagtt tgaagaagcc tatatcccaa aggaacagaa gtattcattc
1920

35 ctgcagaacc cccagacctc cctctgtttc tcagagtcta ttccgacacc ctccaacagg
1980

gaggaaacac aacagaaatc caacctagag ctgctccgca tctccctgct gctcatccag
2040

40 tcgtggctgg agcccgtgca gttcctcagg agtgtcttcg ccaacagcct ggtgtacggc
2100

gcctctgaca gcaacgtcta tgacctcta aaggacctag aggaaggcat ccaaacgctg
2160

45 atggggaggc tggaagatgg cagcccccg actgggcaga ttttcaagca gacctacagc
2220

50 aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg gctgctctac
2280

tgcttcagga aggacatgga caaggctcag acattcctgc gcacgtgca gtgcgctct
2340

55 gtggagggca gctgtggctt ctagggatcc
2370

5 <210> 55
 <211> 786
 <212> PRT
 10 <213> Artificial

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 <222> (391)..(588)

 25 <220>
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 30 <222> (1)..()

 <400> 55
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 Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 40 20 25 30

 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45

 45 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60

 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80
 50 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95

 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 55 100 105 110

 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg

	115	120	125
	Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr		
	130	135	140
5	Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn		
	145	150	155 160
10	Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr		
	165	170	175
	Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe		
	180	185	190
15	Ser Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu		
	195	200	205
	Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe		
	210	215	220
20	Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys		
	225	230	235 240
25	Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser		
	245	250	255
	Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu		
	260	265	270
30	Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro		
	275	280	285
	Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala		
	290	295	300
35	Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile		
	305	310	315 320
40	Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln		
	325	330	335
	Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp		
	340	345	350
45	Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp		
	355	360	365
	Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val		
	370	375	380
50	Glu Gly Ser Cys Gly Phe Ser Trp Gly Gly Gly Gly Ser Phe Pro Thr		
	385	390	395 400
55	Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg		
	405	410	415
	Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr		

	420	425	430
	Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser		
	435	440	445
5	Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr		
	450	455	460
10	Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile		
	465	470	475 480
	Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn		
	485	490	495
15	Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys		
	500	505	510
	Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly		
	515	520	525
20	Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp		
	530	535	540
	Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu		
	545	550	555 560
	Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile		
	565	570	575
30	Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Ser Trp Gly Gly		
	580	585	590
	Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala		
	595	600	605
35	Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln		
	610	615	620
	Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu		
	625	630	635 640
40	Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro		
	645	650	655
45	Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg		
	660	665	670
	Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu		
	675	680	685
50	Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn		
	690	695	700
	Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met		
	705	710	715 720
55	Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln		

	725	730	735
	Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu		
	740	745	750
5	Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val		
	755	760	765
10	Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys		
	770	775	780
	Gly Phe		
	785		
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	<211> 33		
	<212> DNA		
20	<213> Artificial		
25	<220>		
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	33		
35	<210> 57		
	<211> 36		
	<212> DNA		
40	<213> Artificial		
45	<220>		
	<223> synthetic sequence		
	<400> 57		
50	ttaccatgga ttgatcagg cggcggcggga tccaat		
	36		
	<210> 58		
55	<211> 36		

<212> DNA
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 5
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 36
 15
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 <211> 10
 20 <212> PRT
 <213> Artificial
 25
 <220>
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 30 <400> 59
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10
 35 <210> 60
 <211> 48
 <212> DNA
 40 <213> Artificial
 45 <220>
 <223> synthetic sequence
 <400> 60
 50 gccggcggcg gcggatcagg cggcggcggc tcaggcggcg gcggatcc
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 <210> 61
 55 <211> 14

<212> PRT
 <213> Artificial
 5
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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10
 15
 <210> 62
 <211> 43
 20
 <212> DNA
 <213> Artificial
 25
 <220>
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 30
 <400> 62
 ggacatatgc tgtgatcatt cccaaccatt cccttatcca ggc
 43
 35
 <210> 63
 <211> 41
 <212> DNA
 40
 <213> Artificial
 45
 <220>
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 <400> 63
 50
 cgcgaattcg atccatggaa gccacagctg ccctccacag a
 41
 55
 <210> 64
 <211> 36

<212> DNA

<213> Artificial

5

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<400> 64

cgcgctcgacc tagaagccac agctgccctc cacaga
36

15

<210> 65

<211> 602

20

<212> DNA

<213> Artificial

25

<220>

<223> synthetic sequence

30

<400> 65

catatgctgt gatcattccc aaccattccc ttatccaggc tttttgacaa cgctatgctc
60

35

cgcgcccatc gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat
120

atcccaaagg aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca
180

40

gagtctattc cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg
240

ctccgcatct cctgctgct catccagtcg tggtgggagc cegtgcagtt cctcaggagt
300

45

gtcttcgcca acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag
360

50

gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact
420

gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca
480

55

ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca
540

ttcctgcgca tcgtgcagtg ccgctctgtg gagggcagct gtggcttcca tggatcgaat
600

tc
602

<210> 66

10 <211> 192

<212> PRT

15 <213> Artificial

<220>

20 <223> synthetic sequence

<400> 66

25 Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20 25 30

30 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

35 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

40 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

45 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
130 135 140

50 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145 150 155 160

55 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

<210> 67
 5 <211> 600
 <212> DNA
 10 <213> Artificial

 <220>
 15 <223> synthetic sequence

 <400> 67
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 60
 20 cgcgcccatac gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat
 120
 atcccaaagg aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca
 25 180
 gagtctattc cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg
 240
 30 ctccgcatct ccctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt
 300
 gtcttcgcca acagcctggg gtacggcgcc tctgacagca acgtctatga cctcctaaag
 360
 35 gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact
 420
 gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca
 40 480
 ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca
 540
 45 ttctgcgca tcgtgcagtg ccgctctgtg gagggcagct gtggcttcta ggtcgacgcg
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 <210> 68
 50 <211> 192
 <212> PRT
 55 <213> Artificial

<220>

5 <223> synthetic sequence

<400> 68

10 Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20 25 30

15 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

20 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

25 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

30 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
130 135 140

35 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145 150 155 160

40 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190

45 <210> 69

<211> 639

<212> DNA

50 <213> Artificial

55 <220>

<223> synthetic sequence

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 60
 5 cgcgcccatc gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat
 120
 10 atcccaaagg aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca
 180
 gagtctattc cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg
 240
 15 ctccgcatct ccttgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt
 300
 gtcttcgcca acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag
 360
 20 gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact
 420
 gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca
 480
 25 ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca
 540
 30 ttcttgcgca tcgtgcagtg ccgctctgtg gagggcagct gtggcttcgg cggcggcgga
 600
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 639
 35
 <210> 70
 <211> 206
 40 <212> PRT
 <213> Artificial
 45
 <220>
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 50
 <400> 70
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 1 5 10 15
 55 Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 5 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60
 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80
 10 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110
 15 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
 115 120 125
 20 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 130 135 140
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 145 150 155 160
 25 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
 165 170 175
 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190
 30 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 195 200 205
 35 <210> 71
 <211> 630
 <212> DNA
 40 <213> Artificial
 45 <220>
 <223> synthetic sequence
 50 <400> 71
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 60
 cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag
 55 120

gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt
 180
 5 ccgacaccct ccaacagggg ggaaacacaa cagaaatcca acctagagct gctccgcac
 240
 tccctgctgc tcatccagtc gtggtggag cccgtgcagt tctcaggag tgtcttcgcc
 300
 10 aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag
 360
 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc
 420
 15 ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag
 480
 aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc
 540
 20 atcgtgcagt gccgctctgt ggagggcagc tgtggcttcg gcggcggcgg atcaggcggc
 600
 25 ggcggatcag gcggcggcgg atccgaattc
 630
 30 <210> 72
 <211> 206
 <212> PRT
 35 <213> Artificial
 40 <220>
 <223> synthetic sequence
 <400> 72
 45 Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
 1 5 10 15
 Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 20 25 30
 50 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 55 50 55 60
 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser

	65		70		75		80									
	Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser
				85					90						95	
5	Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr
				100					105					110		
10	Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg
			115					120					125			
	Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr
		130					135					140				
15	Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn
	145					150				155						160
	Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr
				165					170					175		
20	Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe
				180					185					190		
25	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly		
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	<210>	73														
	<211>	1248														
30	<212>	DNA														
	<213>	Artificial														
35																
	<220>															
	<223>	synthetic sequence														
40	<220>															
	<221>	misc_feature														
45	<222>	(619)..(1236)														
	<223>	sequence is repeated N-1 times, where N is a positive whole numbe														
50																
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55	tgatcattcc	caaccattcc	cttatccagg	ctttttgaca	acgctatgct	ccgcgcccat										
	60															

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 120

5 gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt
 180

ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcato
 240

10 tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcttcaggag tgtcttcgcc
 300

aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag
 360

15 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc
 420

20 ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag
 480

aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc
 540

25 atcgtgcagt gccgctctgt ggagggcagc tgtggcttcg gcggcggcgg atcaggcggc
 600

ggcgatcag gcggcggcgg atcattccca accattccct tatccaggct ttttgacaac
 660

30 gctatgctcc gcgccatcg tctgcaccag ctggcctttg acacctacca ggagtttgaa
 720

gaagcctata tcccaaagga acagaagtat tcattcctgc agaacccccca gacctccctc
 780

tgtttctcag agtctattcc gacaccctcc aacagggagg aaacacaaca gaaatccaac
 840

40 ctgagagctgc tccgcatctc cctgctgctc atccagtcgt ggctggagcc cgtgcagttc
 900

ctcaggagtg tcttcgcca cagcctgggtg tacgggcct ctgacagcaa cgtctatgac
 960

45 ctccctaaagg acctagagga aggcattcaa acgctgatgg ggaggctgga agatggcagc
 1020

ccccggaactg ggcagatctt caagcagacc tacagcaagt tcgacacaaa ctcacacaac
 1080

gatgacgcac tactcaagaa ctacgggctg ctctactgct tcaggaagga catggacaag
 1140

55 gtcgagacat tctgcgcat cgtgcagtgc cgctctgtgg agggcagctg tggttcggc
 1200

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1248

5 <210> 74
<211> 412
<212> PRT
10 <213> Artificial

15 <220>
<223> synthetic sequence

20 <220>
<221> MISC_FEATURE
<222> (193) .. (398)
25 <223> sequence is repeated N-1 times, where N is a positive whole
numbe

30 <400> 74

Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15
35 Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20 25 30
40 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45
Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60
45 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80
Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95
50 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110
Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125
55 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr

<212> DNA
 <213> Artificial
 5
 <220>
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 10
 <220>
 <221> misc_feature
 15
 <222> (1237)..(1854)
 <223> sequence is repeated N-1 times, where N is a positive whole
 numbe
 20
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 120
 30 gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt
 180
 ccgacacctt ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac
 240
 35 tccctgctgc tcattccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgcc
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 360
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 420
 45 ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag
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 aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc
 540
 50 atcgtgcagt gccgctctgt ggagggcagc tgtggcttcg gggcgggcgg atcaggcggc
 600
 ggcggatcag gcggcgggcg atcattccca accattccct tatccaggct ttttgacaac
 55 660

gctatgctcc gcgcccacg tctgcaccag ctggcctttg acacctacca ggagtttgaa
 720

5 gaagcctata tcccaaagga acagaagtat tcattcctgc agaaccacca gacctccctc
 780

tgtttctcag agtctattcc gacaccctcc aacagggagg aaacacaaca gaaatccaac
 840

10 ctagagctgc tccgcatctc cctgctgctc atccagtcgt ggctggagcc cgtgcagtgc
 900

ctcaggagtgc tcttcgcca cagcctgggtg tacggcgccct ctgacagcaa cgtctatgac
 960

15 ctcttaaagg acctagagga aggcattcaa acgctgatgg ggaggctgga agatggcagc
 1020

ccccgactg ggcatatctt caagcagacc tacagcaagt tcgacacaaa ctacacaaac
 20 1080

gatgacgcac tactcaagaa ctacgggctg ctctactgct tcaggaagga catggacaag
 1140

25 gtcgagacat tcctgcgcat cgtgcagtgc cgctctgtgg agggcagctg tggcttcggc
 1200

ggcgggcgat caggcgggcg cggtacaggc ggcgggcgat cattcccaac cattccctta
 1260

30 tccaggcttt ttgacaacgc tatgctccgc gcccatcgct tgcaccagct ggcctttgac
 1320

acctaccagg agtttgaaga agcctatatc ccaaaggaa agaagtattc attcctgcag
 35 1380

aacccccaga cctccctctg tttctcagag tctattccga caccctcaa caggaggaa
 1440

40 acacaacaga aatccaacct agagctgctc cgcattctcc tgctgctcat ccagtcgtgg
 1500

ctggagcccc tgcagttcct caggagtgtc ttgcgcaaca gcttggtgta cggcgctct
 1560

45 gacagcaacg tctatgacct cctaaaggac ctagaggaag gcatccaaac gctgatgggg
 1620

aggttggaag atggcagccc ccggactggg cagatcttca agcagacctc cagcaagttc
 50 1680

gacacaaact cacacaacga tgacgcacta ctcaagaact acgggctgct ctactgcttc
 1740

55 aggaaggaca tggacaaggc cgagacattc ctgcgcatcg tgcagtgcg ctctgtggag
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ggcagctgtg gcttcggcgg cggcggatca ggcggcggcg gatcaggcgg cggcggatca
 1860

5 ttcccaacca ttcccttata caggcttttt gacaacgcta tgctccgcgc ccatcgtctg
 1920

caccagctgg cctttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag
 1980

10 aagtattcat tctgcagaa ccccagacc tccctctgtt tctcagagtc tattccgaca
 2040

cctccaaca gggaggaaac acaacagaaa tccaacctag agctgctccg catctccctg
 2100

15 ctgctcatcc agtcgtggct ggagcccgtg cagttcctca ggagtgtctt cgccaacagc
 2160

ctgggtgtacg gcgcctctga cagcaacgtc tatgacctcc taaaggacct agaggaaggc
 2220

atccaaacgc tgatggggag gctggaagat ggcagcccc ggactgggca gatcttcaag
 2280

25 cagacctaca gcaagttcga cacaactca cacaacgatg acgcactact caagaactac
 2340

gggctgctct actgcttcag gaaggacatg gacaaggctg agacattcct gcgcctcgtg
 2400

30 cagtgccgct ctgtggaggg cagctgtggc ttctaggctg acgcg
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35 <210> 76

<211> 810

<212> PRT

40 <213> Artificial

45 <220>

<223> synthetic sequence

<220>

50 <221> MISC_FEATURE

<222> (412)..(617)

55 <223> sequence is repeated N-1 times, where N is a positive whole
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5 <220>
 <221> mat_peptide
 <222> (1)..()

10

<400> 76

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 1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 20 25 30

20 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60

25 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95

30 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110

35 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
 115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 130 135 140

40 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
 165 170 175

45 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190

50 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe
 195 200 205

Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala
 210 215 220

55 His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu
 225 230 235 240

	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn	Pro	Gln	
					245					250					255		
5	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu	
				260					265					270			
	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	Leu	Leu	
			275					280					285				
10	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	Val	Phe	
		290					295					300					
	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	Asp	Leu	
15	305					310					315					320	
	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	Leu	Glu	
					325					330					335		
20	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys	
				340					345					350			
	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly	
			355					360					365				
25	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr	Phe	Leu	
		370					375					380					
	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe	Gly	Gly	
30	385					390					395					400	
	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Phe	Pro	Thr	
				405						410					415		
35	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu	Arg	Ala	His	Arg	
				420					425					430			
	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe	Glu	Glu	Ala	Tyr	
			435					440					445				
40	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn	Pro	Gln	Thr	Ser	
		450					455					460					
	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu	Glu	Thr	
45	465					470					475				480		
	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	Leu	Leu	Leu	Ile	
					485					490				495			
50	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	Val	Phe	Ala	Asn	
				500					505					510			
	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	Asp	Leu	Leu	Lys	
			515					520					525				
55	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	Leu	Glu	Asp	Gly	
		530					535					540					

	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys	Phe	Asp	
	545					550					555					560	
5	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly	Leu	Leu	
					565					570					575		
	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr	Phe	Leu	Arg	Ile	
				580					585					590			
10	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe	Gly	Gly	Gly	Gly	
			595					600					605				
	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Phe	Pro	Thr	Ile	Pro	
15		610					615					620					
	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu	Arg	Ala	His	Arg	Leu	His	
	625					630					635					640	
20	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe	Glu	Glu	Ala	Tyr	Ile	Pro	
					645					650					655		
	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn	Pro	Gln	Thr	Ser	Leu	Cys	
				660					665					670			
25	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu	Glu	Thr	Gln	Gln	
			675					680					685				
	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	Leu	Leu	Leu	Ile	Gln	Ser	
30		690					695					700					
	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	Val	Phe	Ala	Asn	Ser	Leu	
	705					710					715					720	
35	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	Asp	Leu	Leu	Lys	Asp	Leu	
					725					730					735		
	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	Leu	Glu	Asp	Gly	Ser	Pro	
				740					745					750			
40	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys	Phe	Asp	Thr	Asn	
			755					760					765				
	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly	Leu	Leu	Tyr	Cys	
45		770					775					780					
	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr	Phe	Leu	Arg	Ile	Val	Gln	
	785					790					795					800	
50	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe							
					805					810							
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55	<211>																593

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 15 cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag
 120
 gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt
 180
 20 ccgacaccct ccaacagggg ggaacacaa cagaaatcca acctagagct gctccgcatc
 240
 25 tccctgtgc tcatccagtc gtggctggag cccgtgcagt tctcaggag tgtcttgcgc
 300
 aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag
 360
 30 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gcccccgac tgggcagatc
 420
 ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag
 480
 35 aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc
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 40 593
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 45 <211> 192
 <212> PRT
 <213> Artificial
 50
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 55 <223> synthetic sequence
 <400> 78

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
 1 5 10 15
 5 Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 20 25 30
 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 10 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60
 15 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95
 20 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110
 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
 115 120 125
 25 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 130 135 140
 30 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 145 150 155 160
 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
 165 170 175
 35 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190
 <210> 79
 40 <211> 592
 <212> DNA
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 45
 <220>
 50 <223> synthetic sequence
 <400> 79
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 55 gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat atcccaaagg
 120

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aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca gagtctattc
180
5  cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg ctccgcatct
240

ccctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt gtcttcgcca
300
10 acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag gacctagagg
360

aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact gggcagatct
15 420

tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca ctactcaaga
480

20 actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca ttcctgcgca
540

tcgtgcagtg ccgctctgtg gagggcagct gtggcttcca tggatcgaat tc
592
25

<210> 80
<211> 191
30 <212> PRT
    <213> Artificial

35
    <220>
    <223> synthetic sequence
40 <400> 80

Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg
1      5      10      15
45 Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu
    20      25      30

Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
50    35      40      45

Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg
    50      55      60
55 Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu
    65      70      75      80

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Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val
 85 90 95
 5 Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp
 100 105 110
 Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu
 115 120 125
 10 Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser
 130 135 140
 Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr
 145 150 155 160
 15 Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe
 165 170 175
 20 Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190
 <210> 81
 <211> 587
 25 <212> DNA
 <213> Artificial
 30
 <220>
 <223> synthetic sequence
 35 <400> 81
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 40 gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat atcccaaagg
 120
 aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca gagtctattc
 180
 45 cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg ctccgcatct
 240
 ccctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt gtcttcgcca
 50 300
 acagcctggt gtacggcgcc tctgacagca acgtctatga cctoctaaag gacctagagg
 360
 55 aaggcatcca aacgctgatg gggaggctgg aagatggcag ccccccggact gggcagatct
 420

tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca ctactcaaga
480

5 actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca ttcttgcgca
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tcgtgcagtg ccgctctgtg gagggcagct gtggcttcta gggatcc
587

10

<210> 82

<211> 191

15

<212> PRT

<213> Artificial

20

<220>

<223> synthetic sequence

25

<400> 82

Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg
1 5 10 15

30

Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu
20 25 30

Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
35 40 45

35

Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg
50 55 60

40

Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu
65 70 75 80

Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val
85 90 95

45

Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp
100 105 110

Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu
115 120 125

50

Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser
130 135 140

55

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr
145 150 155 160

Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe

Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190

5

<210> 83

<211> 1165

10

<212> DNA

<213> Artificial

15

<220>

<223> synthetic sequence

20

<220>

<221> misc_feature

<222> (579)..(1151)

25

<223> sequence is repeated N-1 times, where N is a positive whole
 numbe

30

<400> 83

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35

gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat atcccaaagg
 120

40

aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca gagtctattc
 180

cgacaccctc caacaggag gaaacacaac agaaatccaa cctagagctg ctccgcatct
 240

45

ccctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt gtcttcgcca
 300

50

acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag gacctagagg
 360

aaggcatcca aacgctgatg gggaggctgg aagatggcag ccccgact gggcagatct
 420

55

tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca ctactcaaga
 480

actacggggt gctctactgc ttcaggaagg acatggacaa ggtcgagaca ttctgcgca
 540

5 tcgtgcagtg ccgctctgtg gagggcagct gtggcttctt cccaaccatt cccttatcca
 600

ggctttttga caacgctatg ctccgcgccc atcgtctgca ccagctggcc ttgacacct
 660

10 accaggagtt tgaagaagcc tatatcccaa aggaacagaa gtattcattc ctgcagaacc
 720

cccagacctc cctctgtttc tcagagtcta ttccgacacc ctccaacagg gaggaaacac
 780

15 aacagaaatc caacctagag ctgctccgca tctccctgct gtcattccag tcgtggctgg
 840

20 agcccgtgca gttcctcagg agtgtcttcg ccaacagcct ggtgtacggc gcctctgaca
 900

gcaacgtcta tgacctcta aaggacctag aggaaggcat ccaaacgctg atggggaggc
 960

25 tggaagatgg cagcccccg actgggcaga tcttcaagca gacctacagc aagttcgaca
 1020

caaactcaca caacgatgac gcactactca agaactacgg gctgctctac tgcttcagga
 1080

30 aggacatgga caaggctgag acattcctgc gcatcgtgca gtgccgctct gtggagggca
 1140

35 gctgtggctt ccattggatcg aattc
 1165

<210> 84

40 <211> 191

<212> PRT

45 <213> Artificial

<220>

50 <223> synthetic sequence

<220>

55 <221> MISC_FEATURE

<222> (1)..(191)

<223> sequence is repeated N times, where N is a positive whole number

5

<400> 84

Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg
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10

Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu
20 25 30

15

Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
35 40 45

Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg
50 55 60

20

Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu
65 70 75 80

Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val
85 90 95

25

Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp
100 105 110

Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu
115 120 125

30

Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser
130 135 140

35

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr
145 150 155 160

Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe
165 170 175

40

Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190

<210> 85

45

<211> 2307

<212> DNA

50

<213> Artificial

<220>

55

<223> synthetic sequence

<220>

<221> misc_feature

5 <222> (1153)..(1725)

<223> sequence is repeated N-1 times, where N is a positive whole
numbe

10

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120

20 gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt
180

ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac
240

25 tccttgctgc tcatccagtc gtggctggag cccgtgcagt tcttcaggag tgtcttcgcc
300

30 aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag
360

gaaggcatcc aaacgctgat ggggaggctg gaagatggca gcccccgac tgggcagatc
420

35 ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag
480

aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc
540

40 atcgtgcagt gccgctctgt ggagggcagc tgtggcttct tcccaaccat tcccttatcc
600

45 aggccttttg acaacgctat gctccgcgcc catcgtctgc accagctggc ctttgacacc
660

taccaggagt ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac
720

50 ccccgacct cctctgttt ctcagagtct attccgacac cctccaacag ggaggaaaca
780

caacagaaat ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg
840

55 gagcccgctgc agttcctcag gagtgtcttc gccaacagcc tgggtgtacgg cgctctgac
900

agcaacgtct atgacctcct aaaggaccta gaggaaggca tccaaacgct gatggggagg
 960

5 ctggaagatg gcagcccccg gactgggcag atcttcaagc agacctacag caagttcgac
 1020

acaaactcac acaacgatga cgcactactc aagaactacg ggctgctcta ctgcttcagg
 1080

10 aaggacatgg acaaggtcga gacattcctg cgcacgtgac agtgccgctc tgtggagggc
 1140

agctgtgggt tcttcccaac cattccctta tccaggcttt ttgacaacgc tatgctccgc
 1200

gcccatcgct tgcaccagct ggcctttgac acctaccagg agtttgaaga agcctatatc
 1260

20 ccaaaggaa acgaagtattc attcctgcag aacccccaga cctccctctg tttctcagag
 1320

tctattccga caccctccaa cagggaggaa acacaacaga aatccaacct agagctgctc
 1380

25 cgcactctcc tgctgctcat ccagtcgtgg ctggagcccg tgcagttcct caggagtgtc
 1440

ttgcgaaca gcttgggtga cggcgctct gacagcaacg tctatgacct cctaaaggac
 1500

30 ctagaggaag gcatccaaac gctgatgggg aggctggaag atggcagccc ccggactggg
 1560

35 cagatcttca agcagaccta cagcaagttc gacacaaact cacacaacga tgacgcacta
 1620

ctcaagaact acgggctgct ctactgcttc aggaaggaca tggacaaggc cgagacattc
 1680

40 ctgcgcacgt tgcagtgcg ctctgtggag ggcagctgtg gcttcttccc aaccattccc
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ttatccaggc tttttgacaa cgctatgctc cgcgcccacg gtctgcacca gctggccttt
 1800

gacacctacc aggagtttga agaagcctat atcccaaagg aacagaagta ttcattcctg
 1860

50 cagaaccccc agacctcct ctgtttctca gactctattc cgacaccctc caacagggag
 1920

gaaacacaac agaaatccaa cctagagctg ctccgcatct cctgctgct catccagtcg
 1980

55 tggctggagc ccgtgcagtt cctcaggagt gtcttcgcca acagcctggg gtacggcgcc
 2040

tctgacagca acgtctatga cctcctaaag gacctagagg aaggcatcca aacgctgatg
2100

5 gggaggctgg aagatggcag cccccggact gggcagatct tcaagcagac ctacagcaag
2160

ttcgacacaa actcacacaa cgatgacgca ctactcaaga actacgggct gctctactgc
2220

10 ttcaggaagg acatggacaa ggtcgagaca ttctgcgca tcgtgcagtg ccgctctgtg
2280

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15 2307

<210> 86

20 <211> 192

<212> PRT

<213> Artificial

25

<220>

30 <223> synthetic sequence

<220>

<221> MISC_FEATURE

35 <222> (2)..(192)

<223> sequence is repeated N+2 times, where N is a positive whole
numbe

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<220>

45 <221> mat_peptide

<222> (1)..()

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<400> 86

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	Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn		
	35	40	45
5	Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn		
	50	55	60
10	Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser		
	65	70	75 80
	Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser		
	85	90	95
15	Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr		
	100	105	110
	Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg		
	115	120	125
20	Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr		
	130	135	140
25	Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn		
	145	150	155 160
	Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr		
	165	170	175
30	Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe		
	180	185	190

35

40

45